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ALIGNMENTS

밁 A.Description: involved in protein folding and assembling/disassembling of protein C.Superfamily: heat shock protein 70 C.Superfamily: heat shock protein 70 C.Keywords: ATP; molecular chaperone A;Cross-references: GB:M59828; GB:M34267; NID:g188487; PIDN:AAA63226.1; PID:g188488; C;Function: Immunogenetics 32, 242-251, 1990
A.Title: Structure and expression of the three MHC-linked HSP70 genes.
A.Reference number: A45871; MUID:91055806; PMID:1700760
A.Accession: A45871
A.Schaus: preliminary
A.Schaus: preliminary C;Accession: A45871 R;Milner, C.M.; Campbell, R.D. RESULT 1
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C, Species: Homo saplens (man)
C, Date: 03-Mar-1994 #text_change 20-Aug-1999 õ Ouery Match Best Local Matches 61 Local Similarity ш 1 MAKAAAIGIDIGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60 LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS 120 MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 641; Conservative 100.0%; Score 641; 100.0%; Pred. No. 0; 0; Mismatches DB 2; 0; Length Indels 0; Gaps 60 0;

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KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI 420

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360 360 300 TAYGLDRTGKGERNVLIFDLGGGTFDVSTLTIDDGIFEVKATAGDTHLGGEDFDNRLVNH SMYLTKMKETAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA

TAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH

LNPQNTVFDAKRLIGRKFGDFVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS

SMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSORQATKDAGVIAGLNVLRIINEPTAAA

В

	128 KEIAEAYLGYPYTNAVITVPAYENDSOROATKDAGVIAGLAVLRIINEPTAAAIAYGLDR
	Oy 68 FDAKRLIGRKEGDPVVQSDWKHWPFQVINDSDKFKVQVSYKGETKAFYPBEISSMVLTKM 127
	Oy 8 GIDAGTYSCVOVPOBCKVEITANDGONRTDSEX/AFDDTERLICDANKOVALAROORTV 67
	Query Match 64.3%; Score 412; DB 2; Length 640; Best Local Similarity 99.7%; Pred. No. 0; Matches 632; Conservative 0; Mismatches 1; Indels 1; Gaps
protein compl	ein folding and assembling/disassembling of in 70 erone
	A;Gene: GDB:HSPA1I; HSP70-HOM A;Cross-references: GDB:120058; OMIM:140559 A;Map position: 6p21.3-6p21.3 A;Introns: #status absent C;Function:
	A:Residues: 616-640 https://doi.org/10.1016/j.nib.g32482 ; PIDN:CAA28382.1; PID:g32483 C:Genetics:
	A; Cross-Tereronos: EMBL; XV40/0; NID:9344U; PIDN:CAA285U1.1; PID:9344U1 A; Accession: 137562 A; Status: translation not shown; translated from GB/EMBL/DDBJ
	from GB/EMBL/DDBJ
prepared f	Nucleic Acids Res. 14, 8933-8948, 1986 A.Title: In vitro transcription of a human hsp 70 heat shock gene by extracts A.Reference number: 137561; NUID:87066768; PMID:3786141 A.Recession: 137561
86785	A;Residues: 1-640 <hun> A;Cross-references: GB:M1717; GB:M15432; NID:g184416; PIDN:AAA52697.1; PID:g3867 A;Note: the authors mistranslated residues 463, 491, and 492 R;Drabent, B.; Genthe, A.; Benecke, B.J.</hun>
with the nu	U.S.A. 82, 6455-6459, 1985 wres of eukaryotic hsp70 genes revealed by comparison 160; MUID:86016721; PMID:3931075
	C.Date: 16-Aug-1998 Sequence_revision 02-Jul-1996 #text_change 20-Aug-1999 C.Cacession: A29160; 137561; 137562 R.Hunt, C.; Mocimoto, R.I.
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	Qy 601 OVCNPIISGLYQGAGGPGAGGPGAGGKGGSGSGPTIEETD 641 Db 601 OVCNPIISGLYGGAGGPPGGFGAGGFGGSGGSFTIEETD 641
	Qy 541 ALESYAPNAKSAVEDEGLKOKTSEADKKKYLDKOGEVISHLDANTLAEKDEFEHKRKELE 600 541 ALESYAPNAKSAVEDEGLKOKTSEADKKKYLDKOGEVISHLDANTLAEKDEFEHKRKELE 600
	Oy 481 DANGILAVTA/TOKSTGKANKITITNDKGRIJSKEELERWYQEAEKYKAEDEVQREEVSAKN 540 Db 481 DANGILAVTA/TOKSTGKANKITITNDKGRIJSKEELERWYQEAEKYKAEDEVQREEVSAKN 540
	Oy 421 PYKOPQ1ETYYSDNOPCYLIOVYEGERAMYKONNLLGREELSGIPPA-RGVPO1EVTEDI 480 OD 421 PYKOPQ1ETYTYSDNOPCYLIOVYEGERAMYKONNLLGREELSGIPPA-PRGVPQ1EVTEDI 480 DD 421 PYKOPQ1ETYTYSDNOPCYLIOVYEGERAMYKONNLLGREELSGIPPA-PRGVPQ1EVTEDI 480

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                                                608 SGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD 641
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33357 molecular chaperone hsp70 - bovine
3348 type molecular chaperone hsp70 - bovine
Alternate names: 70K heat shock protein
Species: Bos primigenius taurus (cattle)
Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
Accession: \$53357
Gutierrez, J. A.; Guterriero Jr., V.
Gutierrez, J. A.; Guterriero Jr., V.
Title: Chamical modifications of a recombinant bovine stress-inducible 70 kDa heatReference number: \$53357; MUID:95126904; PMID:7826329
Status: preliminary
Molecule type: mRNA
Residues: 1-641 <GUT>

A;Gene: hap70 G:Function: A.Description: involved in protein folding and assembling/disassembling of protein co G:Superfamily: heat shock protein 70 C:Keywords: ATP: molecular chaperone

denetics:

Cross-references: EMBL:U09861; NID:g497937; PIDN:AAA73914.1; PID:g497938

Matches 470; 198 198 FDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNK 257 258 258 RAVRRIRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPV 317 138 PYTNAVITYPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAAIAYGLDRTGKGERNVLI 197 Local Similarity RAVRRIRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPV 317 FDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNK 257 Conservative 57.7%; 99.8%; 0. Score 370; Pred. No. 0; Mismatches DB 2; Length 641; Indels 0 Gaps 0,

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A;Cross-references: EMBL:M69100
C:GenetLos:
A;Gene: hsp70
C:Function: involved in protein fo
A;Description: involved in protein 70
C;Superfamily: heat shock protein 70
C;Keywords: AfP; molecular chaperone
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A;Reference number: S35718; MUID:92175874; PMID:1339404
A;Accession: S35718
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Pred. No. 1.6e-205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and assembling/disassembling of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 641,
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N.Alternate names: heat shock protein 70
C:species: Carcopithecus aethiops (green monkey, grivet)
C:bate: 13 -Jan 1995 #sequence_revision 13 -Jan 1995 #text_change 20 Aug-1999
C:Accession: S31766; J36927
                                                                                                                                                                                             A;Status: preliminary; translated A;Molecule type: DNA A;Residues; 1-641 <WALL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: X70684; NID: g22781; A; Experimental source: kidney; cell line COS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-638 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Title: The hsc70 gene which is slightly induced by he A:Reference number: 136927; MUID:95080396; PMID:7988690 A;Accession: 136927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-638 <SAI>
R; Residues: 1, angelidis, C.;
FEBS Lett. 355, 282-286, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: S31766
A;Accession: S31766
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                                                       A; Accession: I68986
A; Status: preliminary; translated
A; Molecule type: DNA
A; Residues: 1-641 <WAL2>
                                                                                                                                                                                                                                                     A; Accession: I54542
                                                                                                                                                                                                                                                                           A; Title: Comparative analysis of the three A; Reference number: I54542; MUID:95012453;
                                                                                                                                                                                                                                                                                                                     R; Walter, L.; Rauh, F.; Gunther, Immunogenetics 40, 325-330, 1994
                                                                                                                                                                                                                                                                                                                                                         C;Accession: 154542; 168986; S43388; S47522; 156574; S35955; S38199;
                                                                                                                                                                                                                                                                                                                                                                                                doaK-type molecular chaperone HSP70 - rat
N.Alternate names: dnaK-type molecular chaperone HSP701b; heat shock protein
C:Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: hsp70
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                    A; Cross-references: EMBL: X77208; NID: g927512; PIDN: CAA54423.1;
                                                                                                                                     A; Genetics: HSP1
                                                                                                                                                         A; Experimental source: HSP70
                                                                                                                                                                            A;Cross-references: EMBL:X77207; NID:g1814000; PIDN:CAA54422.1; PID:g450930
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                A; Experimental source: HSP70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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HSP2
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; Pred. No. 1.2e-170;
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NyAlterframane: heat book protein 70
Cypecies. Musamasculus (house nouse)
RyAncessin: Muldorwood S.
Genery, 199-204
NYTELE: Characterization and sequence of a mouse hsp70 gene and it.
A:TELE: Characterization and sequence of a mouse hsp70 gene and it.
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A; Rosidues, 1-70, 'WG', 73-407, 'A()-641 <LIS>
A; Cross-references: EMBL:X74271; NID:93413498; PIDN:CAA52328.1;
A; Note: The authors translated the codon CCG for residue 355 as
R; Longo, F.M.; Wang, S.; Narashimhan, P.; Thang, J.S.; Chen, J.;
J. Neurosci. Res. 36, 325-335, 1933
A; Title: CDNA cloning and expression of stress-inducible rat hsp.
A; Reference number: 156574; NUID:94096443; PMID:8271311
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A.Wolecule type: DNA
A.Residues: 170, NG., 73-109, 'K', 111-203, 'R', 205-261, 'P', 263, 'ADGV',
A.Residues: 170, NG., 73-109, 'K', 111-203, 'R', 205-261, 'P', 263, 'ADGV',
A.Cross-references: EMBL:X75357, NID:g407163; PIDN:CAA53140.1; PID:g
A.Experimental source: ischaemic rat heart
R.Licsowska, K.; Wddlak, W.; Krawczyk, Z.; Wolniczek, P.; Wisniewski,
Biochim. Biophys. Acta 1219, 64-72, 1994
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A;Reference number: $43388; MUID:94190258; PMID:8141767
A;Accession: $43388
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C;Function:
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C;Genetics: <HSP2>
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A;Molecule type: mRNA
A;Residues: 1-256, Dr, 228-641 <LON>
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dnaK-type molecular chaperone
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A; Accession: 156574
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Matches 114
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Matches 101;
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                             Local
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    Conservative
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100.0%; Pr
                         100.0%;
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; Pred. No. 4.6
0; Mismatches
Score 101; DB
; Pred. No. 9.9
0; Mismatches
0;
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                             9.9e-95;
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                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                               Matches
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                                 360 NKSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNST
Similarity
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C;Function:
A;Description: i
C;Superfamily: l
C;Keywords: ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Lowe, D.G.; Moran, L.A.

J. Baol. Chem. 261, 2102-2112, 1986
A; Title: Molecular cloning and analysis of
A; Reference number: A26283, MUID:86111900;
A; Accession: A26283
                                                                                                                                                                                                                                                                                                      C;Date: 31-May-1996 *sequence_revision 31-May-1996 *text_change 20-Aug-1999 (C;Accession: I79546 *Ext_change 20-Aug-1999 (C;Accession: I79546 *Ext_change 20-Aug-1999 (R;Sargent C, C,A; Dunham, I.; Trowsdale, J.; Campbell, R.D. R;Sargent C, C,A; Dunham, I.; Trowsdale, J.; Campbell, R.D. Proc. Natl. Acad. Sci. U.S.A. 86, 1968-1972, 1989 A.Title: Human major histocompatibility complex contains genes for the major A;Reference number: I59139; MUID:89184548; PMID:2538825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: involved in protein for C; Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:M12571; NID:g194014; A; Note: the authors translated the codon CTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dnaK-type molecular chaperone - mouse
N; Alternate names: heat shock protein
                                                                                                                                                                                                                            A; Residues: 1-65 < RE
                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names: chaperonin
C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-420 <LOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: A26283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
                                                                                                                                                                A;Gene: HSP70-2
                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                    A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                        A; Accession: I79540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dnaK-type molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 LLDVAPLSLGLETAGGVMTA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 DLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRYGKGERNVLI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLDVAPLSLGLETAGGVMTA 191
                                                                                ATP;
                                                                                                 heat shock protein 70
                                                                                                                     involved in protein folding and
                                                                                molecular
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                                                                                                                                                                                                        GB:M24744; NID:g188529;
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                 10.1%;
                                                                                chaperone
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HSP70-2; MHC heat shock pr
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                                        Score
                    Score 65;
Pred. No.
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                                                                                                                                                                                                                                                                    GB/EMBL/DDBC
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PMID:2868009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Lv.
J. 2.4e-73;
O;
                                                                                                                                                                                                        PIDN:AAA59845.1; PID:g188530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:AAA57234.1;
For residue 173
1.1e-58;
hes 0;
                                        DB 2;
                                                                                                                        assembling/disassembling of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembling/disassembling of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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Conservative

0,

Mismatches

Indels

0;

Gaps

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daak-type molecular chaperone HSP70.2 - mouse
N.Alternate nammes: heat shock protein 70.2
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cibete: 20 Psb.1995 #sequence_revision 20-Feb-1995 #text_change
Cibete: 20 Psb.1995 #sequence_revision 20-Feb-1995 #text_change
Rizaker1, E.F.; Molgemuth, D.J.; Hunt, C.R.
Mol. Cell. Biol. 8, 225-2332, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
$18211
$18211
dnaK-type molecular chaperone hst70 - rat
dyAlternate names repealed (Norveay rat)
C;pate: 07-sep-1990 #sequence_revision 07-sep-1990 #text_change 30-dan-1998
C;pate: 07-sep-1990 #sequence_revision 07-sep-1990 #text_change 30-dan-1998
C;Accession: $88211
C;Accession: $88211
C;Accession: $88211
                                                                                                                                                                                                                                          A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-633 <WIS>
A; Cross-references: EMBL:X15705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1048, 93-99, 1990
A;Title: Isolation and nucleotide sequence analysis of the rat
A;Reference number: 808211; MUID:90122930; PMID:1688714
A;Accession: 808211
         RESULT
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                                                                                                                                                                                                                                                                                                                A; Gene: HSP70.2
C; Function:
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-633 <ZAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number:
A; Accession: S10859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S10859
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C;Function:
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                                                                                        AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIGIDLGTTYSCVGVFQHGKVEITANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
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                                                                  AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Conser
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 55; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S10859;
                                                                                                                                                                                                                                                                                                                                                                               EMBL: M20567
                                                                                                                                                                             8.6%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUID:88302212; PMID:3405224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence analysis of a new member
                                                                                                                                                        0
                                                                                                                                                                             Score 55;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon
                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                       and assembling/disassembling of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; L
1.5e-47;
                                                                                                                                                                             DB 2; L
1.5e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                        0;
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                    protein comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein comp.
                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
dhaK-type molecular chaperone Hsc70t - mouse
N;Alternate names: heat shock protein 70
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug
C;Accession: 149761
K;Snock, M; Olavesen, M.G.; van Yugt, H.; M
Immunogenetics 40, 159-152, 1994
                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: involved in protein folding and assembling/disassembling of C; Superfamily: heat shock protein 70\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dnaK-type molecular chaperone HSPA2 .
N;Alternate names: heat shock protein
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: the
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-634 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 261, 12692-12699, 1986
A; Title: Organization, nucleotide sequence, and transcription of the chicken
A; Reference number: A25646; WIII:86304452; PMID:3017955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Gallus gailus (chicken)
C;patc: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C;Accession: A2546
C;Accession: A2546
R;Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A25646
dnaK-type molecular chaperone - chicken
------ heat shock protein 70
                                                                                                                                                                                                                                                                                 δã
                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 14g22-14g22
A; Introns: #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number:
A; Accession: A55719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Cloning, sequencing, A; Reference number: A55719; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A55719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB:J02579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A25646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:120059; OMIM:140560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:HSPA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:L26336; NID:g476704; PIDN:AAA52698.1; PID:g476705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Bonnycastle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A55719
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                 6 AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      astle, L.L.C.; Y
23, 85-93, 1994
                                                                                                                                                                                                                                          AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type: DNA: 1-639 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji,
261, 12692-12699, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative (
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu, C.E.; Hunt, C.R.; Trask, B.J.; Clancy, K.P.; Weber,
                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y, and mapping of the human chromosome MUID:95130116; PMID:7829106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID:g211940; PIDN:AAA48825.1; the codon TCG for residue 583
                                                                                                                                                                                                                                                                                                                               t; Score 55; DB
t; Pred. No. 1.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
A2
                     H.; Milner,
                                                               02-Aug-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                    DB 2; L
1.5e-47;
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                        C.M.;
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14 heat shock prote

J.L.;

Indels

0;

Gaps

0

60

as PID:g211941

HSP70

ge

protein

8

Indels

0;

Gaps

0;

protein

G

61 60

Teuscher,

C.;

Campbell,

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RESULT 15

A14115

A1416

A1417

A141
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A;Accession: 149761
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-641 <RES>
A;Cross-references: GB:L27086; NID:g457299; PIDN:AAA59362.1; PID:g457300
C;Genetics:
A;Gene: Hsc70t
C;Anaction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Description: involved in protein 70 C. Superiant, heat shock protein 70 C. Superianily, heat shock protein 70 C. Superianily, heat shock protein 70 C. Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-641 <RES>
A.Cross-references: EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450934
C;Genetics:
Search completed: December 4, 2002, 16:53:11 Job time: 23 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: Hsp70-3
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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C;Superfamily.

C;Keywords: ATP; molecular chaperone
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                     Whatch 8.6%; Score 55; DB 2; L
Local Similarity 100.0%; Pred. No. 1.5e-47;
hes 55; Conservative 0; Mismatches 0;
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hes 55; Conserv
                                                                                                                                                                     6 AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
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100.0%; Pred. No. 1.1
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 641;
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                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                           Gaps
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Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
Published_Applications_AA:*

1 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

2 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

3 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

4 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

5 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

6 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

7 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

8 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

9 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

10 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

11 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

12 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

13 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*

14 /gn2_b/prodata/Jpubpaa/US08_NRW_PUB.pep:*
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length: 2000000000
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867.610 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Res

Sult No.	Score	Query Match	Query Match Length DB	В	ID .	Description
1	. 3263	100.0	641	10	US-09-759-010-3	Sequence 3, Appli
2	3125.5	95.8	642	10	US-09-761-534A-10	10,
w	2859.5	87.6	646	G	US-09-870-759-43	Sequence 43, Appl
4	2859.5	87.6	646	10	US-09-759-010-4	Sequence 4, Appli
5	2740	84.0	665	10	US-09-925-302-724	Sequence 724, App
6	2737	83.9	651	9	US-10-108-605-75	Sequence 75, Appl
7	2039.5	62.5	654	10	US-09-919-172-54	Sequence 54, Appl
8	2010	61.6	653	10	US-09-759-010-2	Sequence 2, Appli
9	1433.5	43.9	660	10	US-09-841-132-446	Sequence 446, App
10	1430.5	43.8	637	10	US-09-815-242-12058	Sequence 12058, A
11	1409	43.2	637	10	US-09-759-010-1	Sequence 1, Appli
12	1409	43.2	638	10	US-09-815-242-10015	-
13	1404	43.0	638	10	US-09-815-242-13713	Sequence 13713, A
14	1399	42.9	620	10	US-09-815-242-11472	Sequence 11472, A
15	1389.5	42.6	610	10	US-09-815-242-5559	Sequence 5559, Ap
16	1389.5	42.6	618	10	US-09-815-242-12567	Sequence 12567, A
17	1389.5	42.6	618	10	US-09-815-242-12970	Sequence 12970, A
18	1388	42.5	635	10	US-09-815-242-11209	Sequence 11209, A
19	1373.5	42.1	609	10	US-09-815-242-10740	Sequence 10740, A

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
131.5	135	140.5	197	231	236.5	248.5	248.5	254	257.5	417.5	467.5	584	593	869	703.5	744.5	790.5	804.5	822.5	860	1040	1067	1334	1334	1373.5
4.0	4.1	4.3	6.0	7.1	7.2	7.6	7.6	7.8	7.9	12.8	14.3	17.9	18.2	21.4	21.6	22.8	24.2	24.7	25.2	26.4	31.9	32.7	40.9	40.9	42.1
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US-09-815-242-5835	US-09-815-242-10779	US-09-815-242-12996	US-09-864-761-42619	US-09-864-761-35578	US-09-864-761-42162	US-09-874-923-49	US-09-991-496-49	US-09-841-132-301	US-09-864-761-36116	US-09-971-536-72	US-09-761-534A-8	US-09-925-301-1519	US-09-801-368-246	US-10-108-605-171	US-09-864-761-34320	US-09-925-302-766	US-09-864-761-34864	US-09-922-217-1102	US-09-731-872-389	US-09-864-761-36258	US-09-761-534A-12	US-09-761-534A-6	US-09-815-242-13682	US-09-815-242-13379	US-09-712-363-162
Sequence 5835, Ap	Sequence 10779, A	Sequence 12996, A	Sequence 42619, A	Sequence 35578, A	Sequence 42162, A	Sequence 49, Appl	Sequence 49, Appl	Sequence 301, App	Sequence 36116, A	Sequence 72, Appl	Sequence 8, Appli	Sequence 1519, Ap	Sequence 246, App	Sequence 171, App	Sequence 34320, A	Sequence 766, App	Sequence 34864, A	Sequence 1102, Ap	Sequence 389, App		Sequence 12, Appl	Sequence 6, Appli	Sequence 13682, A	Sequence 13379, A	Sequence 162, App

ALIGNMENTS

US-09-759-010-3

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LENGTH: 641
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Srivastava, Pramod K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.0%; Score 3263; DB 107.08; Brest Local Similarity 100.0%; Bred No. 3.2e-224; Matches 641; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: STIVESTAVE, PREMOD K.
TITLE OF INVENTION: ORWELEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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CURRENT APPLICATION NUMBER: US/09/759,010
241 FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
                                                                                                             181 IAYGLDRYGKGERNYLIFDLGGGYEDVSILTIDDGIFEVKATRADTHLGGEDEDNRLVNH 240
181 IAYGLDRYGKGERNYLIFDLGGGYEDVSILTIDDGIFEVKATRADTHLGGEDEDNRLVNH 240
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                                                    241 FVEEFKRKHKKDISONKRAVRRLRTACERAKRTLSSSTOASLEIDSLFEGIDFYTSITRA 300
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                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, Jianzhu
APPLICANT: Elsen, Herman N.
APPLICANT: Young, Richard A.
APPLICANT: Young, Richard A.
TITLE OR INVENTION: Protein Pusion Proteins Maps To A Dis
TITLE OR INVENTION: CDA-T Cell Independent
FILE REFERENCE: 0399.2006-033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Richmond, Joan F.J
APPLICANT: Cho, Bryan K.
APPLICANT: Palliser, Deborah
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 60/176,143
PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/761,534A
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                                                                                                                                                                                                                                                                                                                     LENGTH: 64
TYPE: PRT
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                                                               LNPQNTVFDAKRLIGRKFGDAVVQSDMKHWPFQVVNDGDKPKVQVNYKGESRSFFPEEIS
                                                                            LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
                                                                                                                            MAKNTAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
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KSINPDEAVAYGAAVQAAILMGDKSENVODLLLLDVAPLSIGGEFFAGGVMFALIKRNSTI
KSINPDEAVAYGAAVQAAILMGDKSENVODLLLLDVAPLSIGGEFFAGGVMFALIKRNSTI
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                       95.8%; Score 3125.5;
95.2%; Pred. No. 1.90
tive 20; Mismatches
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1.9e-214;
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                                                                                                                                                    PTKQTQTFTTYSDNQPGVLIQVYEGERAMTRDNNLLGRFELSGIPPAPRGVPQIEVTFDI
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; ORGANISM: Homo sapiens US-09-870-759-43 US-09-870-759-43 SOFTWARE: PatentIn version 3.1 SEQ ID NO 43 LENGTH: 646 Sequence 43, Application U Patent No. US20020177551A1 GENERAL INFORMATION: CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166 CURRENT APPLICATION NUMBER: US/09/870,759 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE FILE REFERENCE: 870759 APPLICANT: TERMAN, David S TYPE: PRT US/09870759

밁 В DЬ 밁 δÃ Q δÃ Matches Query Match Best Local 181 181 121 121 61 61 Local Similarity MAKAAAIGIDLGTTYSCYGYFQHGKYEIIANDQGNRTTPSYYAFTDTERLIGDAAKNQVA 60 IAYGLDKKVGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNH IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH SWYLTRAKEIAEAYLGKTYTNAVYTYPAYENDSOROATKOAGYJAGLIVYLRIINEPTAAA 180 MNPTNTVFDAKRLIGRRFDDAVVQSDMKHWPFMVVNDAGRPKVQVEYKGETKSFYPEEVS 120 LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS 120 MSKGPAVGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60 Conservative 87.6%; 48; Score 2859.5; DB 9; Pred. No. 1.5e-195; 8; Mismatches 40; Indels 5 Gaps 240 240

Length 646;

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; LENGTH: 646
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; ORGANISM: Homo sapiens
US-09-759-010-4
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SEQ ID NO 4
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Patent No. US20010034042A1
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STIVUSEAVA, PRAMOG K.
TITLE OF INVENTION: COMPLEXES OF PEPTIDE BI
TITLE OF INVENTION: PROTEINS AND THEIR USE
FILE REFERENCE: 8449-115
CURRENT APPLICATION NUMBER: US/09/759,010
CURRENT FILLING DATE: 2001-01-12
NUMBER OF SED ID NOS: 11
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                   FVEEPKRKHKKDISONKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300
                                                                                                                                                                                                                          LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPPQVINDGDKPKVQVSYKGETKAFYPEEIS 120
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FIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRA
                                                                                      IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
                                                                                                                                      SMVLTKMKETAEAYLGKTVTNAVVTVPAYFNDSQRQATKDAGTTAGLNVLRIINEPTAAA
                                                                                                                                                                        SMYLTKMKEIAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA 180
                                                                                                                                                                                                         MNPTNTVFDAKRLIGRRFDDAVVQSDMKHWPFMVVNDAGRPKVQVEYKGETKSFYPEEVS
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                                                                   TAYGLUKKVGAERNVLIFDLGGGTFDVSTLTTEDGIFEVKSTAGDTHLGGEDFDNRMVNH
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                                                                                                                                                                                                                                                                                                                                                                 87.6%;
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LOCATION: (216)
COTHER INFORMATION: >
NAME/KEY: SITE
LOCATION: (298)
COTHER INFORMATION: >
US-09-925-302-724
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NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 724
LENGTH: 665
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US00/05918 PRIOR FILING DATE: 2000-03-08
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ORGANISM: Homo
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                      KMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGL 185
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TVFDAKRLIGRKFADTTVQSDMKHWPFRVVSEGGKPKVRVCYRGEDKTFYPEEISSMVLS
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Pred. No. 4.7e-187;
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US-10-108-605-75
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Matches
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LENGTH: 651
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                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kamdar Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANGASTER THAT ENCODE
TITLE OF INVENTION: PROFEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
TILE REPERENCE: 31133B ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
CURRENT APPLICATION UNMEER: US/10/108,605
CURRENT PILING DATE: 2002-03-27
PRIOR APPLICATION UNMEER: US/761.142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION UNMEER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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181 IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
                                                                          121 SMYLTKMKETAEAYLGYPYTNAVITVPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA 180
                                                                                                                61 MNPTQTIFDAKRLIGRKFDDAAVQSDMKHWPFEVVSADGKPKIEVTYKDEKKTFFPEEIS
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                                      SMVLTKMKETAEAYLGKTVTNAVITVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAA
                                                                                                                                                    LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
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                                                                                                                                                                                                                                                                                  Similarity
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Bachmann, Jane
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                                                                                                                                                                                                                                                                83.9%; Score 2737; |
81.3%; Pred. No. 7.5
tive 55; Mismatches
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7.5e-187;
nes 57;
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PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOPTWARE: PERL Program
SEQ ID NO 54
LENGTH: 654
                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. US20020119463A1
                                                                                                                                                                                                                               Matches 398;
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APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKE
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                               LDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEE
                                 TKMKETAEAYLGKKVTHAVVTVPAYFNDAQRQATKDAGTTAGLNVMRIINEPTAAAIAYG
                                                  TKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYG 184
                                                                                                 TVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSY-KGETKAFYPEEISSMVL 124
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                             Score 2039.5; DB 1
Pred. No. 2.6e-137;
                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                          DB 10; Length 654;
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CURRENT APPLICATION NUMBER: US/09/759,010
CURRENT FLING BATE: 2001-01-12
NUMBER OF SEQ ID NOS: 11
SOPTWARE: Perentin Ver. 2.1
SEQ ID NO 2
LENGTH: 63
TIPE: PRT
GREANISM: Homo sapiens
US-09-759-010-2
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Best Local :
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: STIVASTAVA, PRAMOD K.
TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
TITLE OF INVENTION: PROFEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
FILE REFERENCE: 8449-135
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31 VGIDLGTTYSCYCVPONGKYVEILANDGGNRTFPSYVAFT-DEGERLIGDAKNOLTSNPEN 90
FKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEE
                                                      LDKR-EGEKNILVFDLGGGTFDVSLLTIDNGVFEVVATNGDTHLGGEDFDQRVMEHFIKL
                                                                          LDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEE
                                                                                                                               TKMKETAEAYLGKKVTHAVVTVPAYFNDAQRQATKDAGTIAGLNVMRIINEPTAAAIAYG
                                                                                                                                                               TKMKEIAEAYLGYPYTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYG
                                                                                                                                                                                                  TVFDAKRLIGRTWNDPSVQQDIKFLPFKVVEKKTKPXIQVDIGGGQTKTFAPEEISAMVL
                                                                                                                                                                                                                                   TVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSY-KGETKAFYPEBISSMVL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPIISKLY-GSAGPPPTG 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPIISGLYQGAGGPGPGG 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAYSIKNQIGDKEKLGGKLSSEDKETMEKAVEEKIEWLESHQDADIEDEKAKKKELEEIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAFNMKSAVED-EGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKIKAEDEVQRERVSAKNALES 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQIFSTASDNQPTVTIKVYEGERPLTKDNHLLGTFDLTGIPPAPRGVPQIEVTFEIDVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDIDANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVWTALIKRNSTIPTKQ 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNMDLFRSTMKPVQKVLEDSDLKKSDIDETVLVGGSTRIPKIQQLVKEFFNGKEPSRGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSIN 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKKKTGKDVRKDNRAVQKLRREVEKAKRALSSQHQARIEIESFYEGEDFSETLTRAKFEE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDKR-EGEKNILVFDLGGGTFDVSLLTIDNGVFEVVATNGDTHLGGEDFDQRVMEHFIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILRVTAEDKGTGNKNKITITNDQNRLTPEEIERMVNDAEKFAEEDKKLKERIDTRNELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDEAVAYGAAVQAGVLSGD--QDTGDLVLLDVCPLTLGIETVGGVMTKLIPRNTVVPTKK 447
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                63.9%; Score 2010; DB 10; 63.9%; Pred. No. 3.2e-135;
                                                                                                                                                                                                                                                                                                                                                 104; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                    653;
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244 KQEGIDLSKDNMALQRLKDAAEKAKIELSG--VSSTEINQPFITIDANGPKHLALTLTRA

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243 246 185

RKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGID-----FYTSITRA K--EGDKKIAVFDLGGGTFDISILEIGDGVFEVLSTNGDTHLGGDDFDGVIINWMLDEFK RTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFK MKETAEAYLGETVTEAVITVPAYFNDSQRASTKDAGRIAGLDVKRIIPEPTAAALAYGID MKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLD 186

RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN 360

247

186 187 126 127

71 LASTKRFIGRKFSE--VESEIKTVPYKV---APNSKGDAVFDVEQKLYTPEEIGAQILMK

125

VFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTK 126

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US-09-841-132-446
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                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SED ID NOS: 599
SOFTMARE: FASTSEQ FOR WINDOWS VETSION 3.0/4.0
SED ID NO 345
LENGTH: 660
TYPE: PRT
ORGANISM: Chlamydia trachomatis serovar D
ORGANISM: Chlamydia trachomatis serovar D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 446, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
                                                                                                        Matches
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION. DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
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                                                                                                                            Match 43.9%; Score 1433.5; DB Local Similarity 48.2%; Pred. No. 2.9e-94;
                                 7 IGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPIISKLY-GSAGPPPTG
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SQIFSTASDNQPTVTIKVYEGERPLTKDNHLLGTFDLTGIPPAPRGVPQIEVTFEIDVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDEAVAYGAAVQAGVLSGD--QDTGDLVLLHVCPLTLGIETVGGVMTKLIPSNTVVPTKN 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAYSLKNQIGDKEKLGGKLSSEDKETMEKAVEEKIEWLESHQDADIEDFKAKKKELEEIV 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAFNMKSAVED-EGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVC
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                                                                                                    318;
                                                                                                    Conservative 113;
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                                                                                                        Mismatches
                                                                                                                                                   DB 10; Length 660;
                                                                                                    186;
                                                                                                        Indels
                                                                                                        43;
                                                                                                    Gaps
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US-09-815-242-12058
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US-09-815-242-12058
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION UNBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION UNBER: 60/24/3,78
PRIOR APPLICATION UNBER: 60/23,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 12058
LENGTH: 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12058, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/91,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICAMY: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
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            66 TVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLT 125
                                                                                                                                                                         Local Similarity
                                                                                                     IGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFT-DTERLIGDAAKNQVALNPQN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OFEHLASSLIERTKOPCAQALKDAKLSASDIDDVLLVGGMSRMPAVQAVVKEIF-GKEPN
                                                          IGIDLGTTNSCVAILENGNVKVIENAEGARTTPSIIAYTNDGETLVGQPAKRQAVTNPQN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALESYAFIMKSAVEDEGLKGKISEADKKKV---LDKCQEVISWLDANTLAEK---DEFE- 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HMQKIGEAMQAQSASAAASSAANAQGGPNINSEDLKKHSFSTRPPAGGSASSTDNIEDAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind, Judith W. Wall, Daniel Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Robert T.
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                                                                                                                                                Conservative 106;
                                                                                                                                             43.8%; Score 1430.5; DB 10; Length 49.5%; Pred. No. 4.5e-94; tive 106; Mismatches 179; Indels
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7 IGIDLGTTYSCYGVFQHGKVEIIANDQGNRTTPSYVAFT-DTERLIGDAAKNQVALNPQN 65

IGIDLGTTNSCVALMDGTTPRVLENAEGDRTTPSIIAYTQDGETLVGQPAKRQAVTNPQN 63
TVFDAKRLIGRKFGDPVVQSDMKHWPFQVI--NDGDKPKVQVSYKGETKAEYPEEISSMV 123

TLFAIKRLIGRRFQDEEVQRDVSIMPFKIIAADNGD---AWVEVKGQKMA--PPQISAEV 118

124 LTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAY 183

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                                                                                           ; ORGANISM: Homo sapiens
US-09-759-010-1
                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Vei
SEQ ID NO 1
LENGTH: 637
TYPE: PRT
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US-09-759-010-1
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                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SIYUSELVA, Pramod K.
APPLICANT: SIYUSELVA, Pramod K.
TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOO
TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHEKAPEUTIC AGENTS
FILE REFERENCE: 6449-135
                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09759010 Patent No. US20010034042A1
      Matches 314; Conservative
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/759,010
CURRENT FILING DATE: 2001-01-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDIDANGILHVSAKDKATGKQQSIVIKASSG-LSEDEIQQMVRDAEANAEEDRKFEELAA
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                                                                                                                                                                                                      Patentin Ver.
                        43.2%; Score 1409; DB 10; 51.0%; Pred. No. 1.5e-92;
      91;
      Mismatches 175;
                                                                                                                                                                                                                                                                                                                                      PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
      Indels 36;
                                          Length 637;
Gaps
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                                                               SEQ ID NO 10015
                                                                                                                                                               PRIOR APPLICATION NUMBER: 66/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR RILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION. PROKATYCES
FILE REFERENCE: ELITEA, 011A.
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT EILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                      PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                    TYPE: PRT
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ORGANISM: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKEPRKDVNPDEAVAIGAAVQGGVLTGD----VKDVLLLDVTPLSLGIETMGGVMTTLIA 412
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Xu, H. Howard
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TITLE OF INVENTION: identification of ES
TITLE OF INVENTION: PROMITYONE
ETLE REFERENCE: ELITER, 011A,
CURRENT ADDICATION NUMBER: US/09/815,24
CURRENT PILING DATE: 2001.03-21
PHION PILING DATE: 2000-03-21
PHION FILING DATE: 2000-03-21
PHION FILING DATE: 2000-03-24
PHION FILING DATE: 2000-05-23
PHION FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-815-242-13713
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                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Sequence 13713, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith
                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 YLVEEFKKDQGIDLRNDPLAMQRLKEAAEKAKIELSSAQQTDVNLPYITADATGPKHMNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 HFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGI----DFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 LTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAY 183
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                                                                                                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Mismatches 175;
                                                                                                                                                                      Essential
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RESULT 14
US-09-615-242-11472
US-09-615-242-11472, Application US/09815242
Sequence 11472, Application US/09815242
Patent No. US20020061559A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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US-09-815-242-13713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13713
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PRIOR FILING DATE: 2000-12-25
PRIOR PRIOR TRANSPERS: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SED ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING BATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KMKEIABAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFT-DTERLIGDAAKNQVALNPQN 65
                                                                                                                                                                                                                                                                         TRNQGDHLLHSTRKQVEEAG -- DKLPADDKTAI ---- ESALSALETALKGEDKAAIEAKM
                                                                                                                                                                                                                                                                                                                                                                           FDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERWVQEAEKYKAEDEVQRERVS
                                                                                                                                                                                                                                                                                                                                                                                                                          TTIPTKHSQVESTAEDNQSAVTIHVLQGERKRASDNKSLGQFNLDGINPAPRGMPQIEVT
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                                                                                                                                                                                                                                                                                                             AKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAE-KDEFEHKR 596
                                                                                                                                                                                                                                                                                                                                                 FDIDADGILHVSAKDKNSGKEQKITIKASSG-LNEEEIQKMVRDAEANAESDRKFEELVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRAKLESLVEDLVNRSIEPLKVALQDAGLSVSDINDVILVGGQTRMPMVQKKVAEFF-GK
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IPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFD NKSVNPDEVVAVGASIQGGVLKGD----VKDVLLLDVTPLSLGIETLGGVMTKVIDRGTT

479 411 419 355

471

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356 360 297 300 239 246 181

ARFEELCSDLFRSTLEFVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDL 359

KNETGIEIKNDVMALQRLKEAAENAKKELSSAMET - - EINLPFITADATGPKHLVKKLTR KRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGID-----FYTSITR

296 299 238

NKSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNST AKFESLTEDLVEETISKIESVIKDAGLTKNEISEVVMVGGSTRIPKVQERVKAFIN-KEL

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IDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAK 539

IDANGILTVSAQDKNTGKSQEIKISGSSG-LSDSEIEKMVKDAELHKEEDARKKEVIEAR IPAKKSQVFSTAEDNQPAVSIMVLQGERELARDNKSLGKFDLQGIAPAPRGMPQ1EVTFD

530

472 480 B

DK--KESEKIMYYDLGGGTFDVTVLETGDNVVEVLATGGDAFLGGDDFDNRVIDFLAAEF

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US-09-815-242-11472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR PILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/250-648

PRIOR PILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: 60/257,727

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-22-42,578

PRIOR PILING DATE: 2000-10-23-6,55

PRIOR PILING DATE: 2000-10-23-6,55

PRIOR PILING DATE: 2000-11-22-26,591

PRIOR PILING DATE: 2000-12-22-6,591

PRIOR PILING DATE: 2000-12-22-6,591

PRIOR PILING DATE: 2000-12-22-6,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11472
LENGTH: 620
                                                                                                                                                                                                                                                                                                                   Ouery Match 42.9%; Score 1399; DB 10)

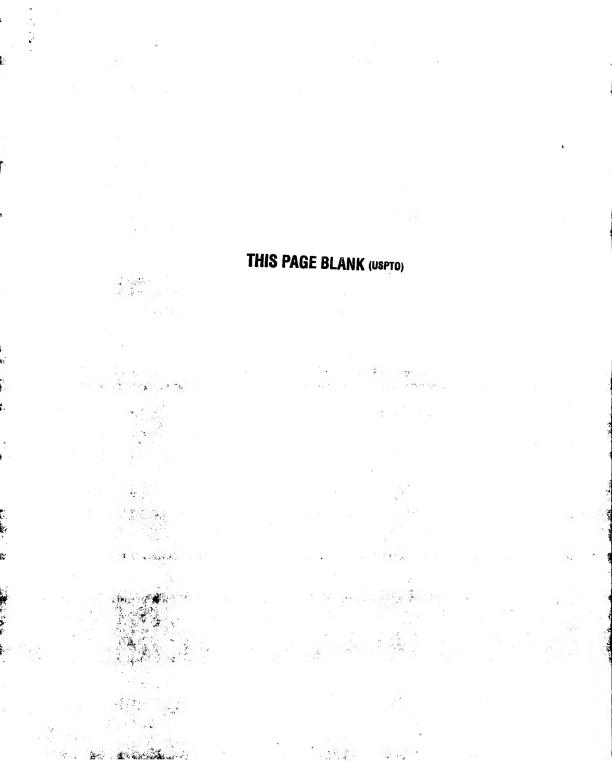
Best Local Similarity 48.0%; Peck. No. 7.4e-92;

Matches 293; Conservative 115; Mismatches 177;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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               186
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DRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEF
                                                                                                   KMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGL 185
                                                                                                                                             TIYSIKRIMGLMFNEDKAKEAEKRLPYKIVDRNGACAIEIS----GKIYTPQEISAKILM
                                                                                                                                                                                    TVFDAKKLIGKKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLT 125
                                                                                                                                                                                                                                                      IGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDT-ERLIGDAAKNQVALNPQN
                                                         KLKEDAESYLGESVTEAVITVPAYFNDSQRKATKEAGTIAGLNVLRIINEPTSAALAYGL 180
                                                                                                                                                                                                                                 IGIDLGTTNSAMAYYEGNEAKIIANKEGKNTTPSIVAFTDKGEILVGESAKRQAVTNPEK
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/291,078
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/257,931
PRIOR PELICATION NUMBER: 60/257,931
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US-09-815-242-5559
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Best Local 9
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELTTRA.011A
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                                                                                    157 KTDKDEK-VLVFDLGGGTFDVSILELGDGVFEVLSTAGDNKLGGDDFDQVIIDYLVAEFK
216 KENGVDLSQDKMALQRLKDAAEKAKKDLSGVSQTQISLPFISAGENGPLHLEVNLTRSKF
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Local Similarity 47.3%; Pred. No. 3 4e-91;
Nes 302; Conservative 111; Mismatches 179; Indels 47;
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                                                                                                         RTGKGERNYLIFDLGGGTFDVSILTIDDGIFFYKATAGDTHLGGEDFDNRLVNHFYEEFK 246
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                                       RKHKKDISQNKRAVRRLRTACERAKRTLS -- SSTQASLEIDSLFEG -- IDFYTSITRARF 302
                                                                                                                                                                                                                                                                                                         VFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTK 126
                                                                                                                                                                                                                                                                                                                                                IGIDLGTTNSCVTVLEGDEPKVIQNPEGSRTTPSVVAFKNGETQVGEVAKRQAITNP-NT
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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                                                                                              510 DSLYFQVEKTLTDLG--ENIGEEDKKSAEEKKDALKTALEGQDI---EDIKSKKEELEKV 564
                                                                                                                                                 543 ESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQV 602
                                                                                                                                                                                                451 NGIVNVTAKDLGTNKEQRITIQSSSS-LSDEEIDRMVKDAEVNAEADKKRREEVDLRNEA
                                                                                                                                                                                                                                                                                               391 SKSQIYSTAVDNQPSVDVHVLQGERPMAADNKTLGRFQLTDIPPAERGKPQIEVTFDIDK 450
                                                                                                                                                                                                                                                                                                                                                                                             335 VNPDEVVAMGAAIQGGVITGD----VKDVVLLDVTPLSLGIEILGGRMNTLIERNTTIPT
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IQELSAKVYEQAAQQQQ----QAQGANAGQNNDSTVEDAE
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Search completed: December 4, 2002, 16:44:35 Job time: 14 secs



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EVEEFKRKHKKDISQNKRAVRLRTACERAKRILSSSTQASLEIDSLFEGIDFYTSITRA

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MNPTNTVFDAKKLIGRRFDDAVVQSDMKHWPFMVVNDAGRPKVQVEVKGETKSFYPEEVS LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS

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Ouery Match 87.5%; Score 286.5; DB 1; Length 646; Best Local Similarity 85.6%; Preed, No. 67-225; Matches 553; Conservative 47; Mismatches 41; Indels 5; Gaps 3; Oy 1 MAKANAIGIDLGTTYSCYGVFOHGKVEIIANDGGNETTPSYVAFTDTERLIGDAKNOVA 60	TELECOMONICATION INFORMATION: TELEPHONE: 516-742-434 TELEPHONE: 516-742-436 TELEPAX: 516-742-436 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHRACTERISTICS: LENGTH: 646 milno acidd TYPE: amino acidd TYPE: mino acidd TYPE: protein	AJ PF CC	CITY: GATCHE CITY PLAZA CITY: GATCH CITY STATE: NY COUNTRY: USA 2.P: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LBM PC COMPATIBLE COMPUTER: LBM PC C	Sequence of the control of the contr	Db 605 KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVIPLSLGIETAGGVMTVLIKRNTI 664 QY 421 PTKQTQIFTYSONQPGVLLQVYEGERAMYKNUNLGREEGEGFPARRGVPQLIVTEPDI 480
PRIOR APPLICATION NUMBER: US 60/011,491 APPLICATION NUMBER: US 60/011,491 APPLICATION NUMBER: US 60/011,491 ATTORREY/AGENT INFORMATION: NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERRANCE/DOCKET NUMBER: PCE 3165 TELECOMMUNICATION INFORMATION:	COUNTRY: California COUNTRY: United States COUNTRY: United States COUNTRY: United States COMPUTER READ-BLE FORM: COMPUTER: IEM TO COMPATE THE TO COMPATE THE TO THE THE TO	RESULT 3 US-08-797-358B-3 Sequence 3, Application US/08797358B FRIENT NO. 626447B GENERLI INFORMATION: APPLICANT: Adams, John TITLE OF INVENTION: INFRACELLULAR VITAMIN D BINDING PROTEIN UNMER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSE: Campbell & Flores LLP STREET: 4370 La Johla Village Drive, Suite 700 CITY: San Disco	Oy 541 ALESYAPMKSAVEDECIKCK ISEADKKKYLDKOGEVISKLDANTIAEKDEFEHKRKELE 600	OY 361 KSINDBANAYGAANGAAILMGDKSENVODLLILDVAPLSIGLETAGGVMTALIKRNSTI 420	OY 61 LNEONTYDDAKRLIGRKFGDPWGSDHKHWPFOYINDGDKFKVOVSIKGETKAPYPEEIS 120 61 NRTHINGTHINGTHINGTHINGTHINGTHINGTHINGTHING

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                                                                                                GENERAL INFORMATION:
                                                                                                               Sequence 36, Application US/09632538C Patent No. 6440674
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Best Local
APPLICANT: Misro; Sentosh et al.
TITLE OF INVENTION: LANT PROMOTER DERIVED
TITLE OF INVENTION: ITS USE
ELLE REFERENCE: 54350
CURRENT APPLICATION NUMBER: US/09/632,538C
CURRENT APPLICATION NUMBER: US/09/632,538C
UNMBER OF SEQ ID NOS: 37
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SEQUENCE CHARACTERISTICS:
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Similarity 81.6%;
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Pred. No. 1.6e-213;
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US-09-632-538C-36
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                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                             Sequence 16, Application US/08441139 Patent No. 5773245
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                                                                                                                                                                GENERAL INFORMATION:
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TYPE: PRT
                                                                             APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Roblison, Ame S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION
TITLE OF INVENTION: RECONSINANTLY EXPRESSED PROTEINS
NUMBER OF SECRET 200
CORRESPONDENCE ADDRESS:
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     COUNTRY: USA
ZIP: 11530
                                            STREET: 400 Garder
CITY: Garden City
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les 402; Conservative
                               STATE:
                                                                      ADDRESSEE:
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                                                       E: SCULLY, SCOTT, MURPHY
400 Garden City Plaza
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246 KRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEEL
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                                                                                                                  QIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDIDANGI
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                                                                                          QVFTTYQDQQTTVSIKVYEGERSLTKDCRELGKFDLSGIPPAPRGVPQIEVTFEVDANGI
                                                                                                                                                                                        DEAVAYGAAVQGGILSGEGGDETKDILLLDVAPLSLGIETVGGVMTKLIPRNTVIPTKKS
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Pred. No. 3.5e-162;
8; Mismatches 114;
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; MOLECULE TYPE: protein US-08-441-139-16
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Best Local Similarity 64.7%; Pred, No. 3.1e-159;
Matches 400; Conservative 105; Mismatches 106; Indels
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REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION: TELEPHONE: 515-742-433
TELEPK: 516-742-4366
TELEX: 230 001 0000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, FRANK S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy
   580
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                                                                                                                       ILNYTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNALES 544
                                                                                                                                                                                                                                                                                                                           PDEAVAYGAAVQAAILMGDKSENVQDLLLLLDVAPLSLGLGTAGGVMTALIKRNSTIPTKQ 424
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YAYSEKNQIGDKEKEGGKESSEDKETIEKAVEEKIEWEESHQDADIEDFKSKKKELEEVV 639
                                            YAFNMKSAVED-EGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVC
                                                                                               ILRVTAEDKGTGNKNKITITNDQNRLTPEEIERMVNDAEKFAEEDKKLKERIDARNELES
                                                                                                                                                                                               SQIESTASDNQPTVTIKVYEGERPLTKDNHLLGTFDLTGIPPAPRGVPQIEVTFEIDVNG
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                                                                                                                                                                                                                                               TQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDIDANG 484
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                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 06-JUL-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                      211
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                 245 FKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEE 304
                                                                                        185
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                                                                                                                                                           125 TKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                               91 TYFDAKRLIGRTWNDPSVQQDIKFLPFKVVEKKTKPYIQVDIGGGQTKTFAPEEISAMVL 150
                                                                                                                                                                                                                                                                    31 VGIDLGTTYSCVGVFKNGRVEIIANDQGNRITPSYVAFTPEGERLIGDAAKNQLTSNPEN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DiGiglio, Frank S
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                                                                    LDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEE 244
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400 Garden City Plaza
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                                                                                                                                                                                                                                                                                                                                            Conservative 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linear
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METHODS FOR INCREASING SECRETION OF RECOMBINANTLY EXPRESSED PROTEINS
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Pred. No. 2e-158;
                                                                                                                                                                                                                                                                                                                                            Mismatches 108; Indels
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US-08-441-139-2
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                                                                                                                                                                                               APPLICATION NUMBER: USYON FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION HUMBER: NO OF FILING DATE: 06-JUL-1993
ATTORNEY/AGRMT INFORMATION:
MAMBE: DIGIGITON HUMBER: 31,34
REGISTRATION HUMBER: 31,34
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                                                                              TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                               REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                TYPE: amino acid TOPOLOGY: linear
                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                            NUMBER: US/08/441,139
15-MAY-1995
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Query Match

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                                                                                                                                                                                                                                                                                Sequence 5, Application US/08441139
Patent No. 577245
GEMERAL INFORMATION:
APPLICANT: MATEUR, Dr. Karl D.
APPLICANT: MADDINGON, ARNE S.
APPLICANT: MADDINGON, ARNE S.
TITLE OF INVENTION: MECHANICA EXPRESSED PROTEINS
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 62.9%;
Matches 388; Conservative 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
                                                  COMPUTER READABLE FORM:
MEDIUM TWEE: Flopy disk
COMPUTER: JEM PC COMPAELIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                             NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
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                                                                                                                                       ZIP:
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                                                                                                                                                                             STREET: 400 Garde
CITY: Garden City
STATE: NY
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                                                                                                                                                            COUNTRY:
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2; Mismatches 122;
                                                         #1.25
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Matches
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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PROG APPLICATION NUMBER: US 08/089
PILING DATE: 06-JUL-1993
ATTORNEY_AGENT INFORMATION:
NAME: DIGIGION NUMBER: 31,346
REFERENCE_/DOCKET NUMBER: 8646
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TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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                                                                                                                                            517 QIEVTFALDANGILTVSATDKDTGKSESITIANDKGRLSQDDIDRMVEEAEKYAAEDAKF
                                                                                                                                                                                                                                                      413 LIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVP 472
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                                                                                               RERVSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANT-LAEKDE
                                                                                                                                                                 QIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQ
                                   FEHKRKELEQVCNPIISGLYQGAGGPGPGGF 622
                                                                         KAKSEARNTFENFYHYVKNSVNGE-LAEIMDEDDKETVLDNVNESLEWLEDNSDVAEAED
                                                                                                                                                                                                                      LIKRNTAIPTKKSQIFSTAVDNQKAVRIQVYEGERAMVKDNNLLGNFELSDIRAAPRGVP
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FEEKMASFKESVEPILAKASASQGSTSGEGF 666
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RESULT 9 US-08-441-139-7

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Best Local
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-JUL-1993
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MEDIUM TYPE: Floppy disk:
COMPUTER: BIM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Kelease #1.0.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
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APPLICATION NUMBER: US
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NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
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APPLICANT: Robinson,
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CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
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TELEFAX: 516-742-4366
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EAVAYGAAVQAGVLSGE--EGSDNIVLLDVIPLTLGIBTTGGVMTKLIGRNTPIPTRKSQ
                               EAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQ
                                                                                                                                                                RKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEELC
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                                                                                                                                                                                                                               RIGKGERNVLIFDLGGGIFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEDEK 246
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                                                                                                                                                                                                                                                                                                                                                       IFDIKRLIGRKFDEKTMAKDIKSFPFHIVNDKNRPLVEVNVGGKKKKFTPEEISAMILSK 157
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                                                                                                                                          RKNNVDVTKDLKAMGKLKREVEKANGTLSSQKSVRIEIESFFNGQDFSETLSRAKFEEIK 336
                                                                                                                                                                                                                                                                                  MKQTAEAYLGKPYTHSYVTVPAYFNDAQRQATKDAGTIAGLNVIRIVNEPTAAAIAYGLD
                                                                                                        SDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.1%; Score 1897; DB 1; 59.5%; Pred. No. 1.6e-146;
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Qy 3 KAAAIGIDLGTTYSCVGVFOHGKVEIIANDQGNRTTPSYVAFT-DTERLIGDAAKNQVAL 61	Ouery Match 45.2%; Score 1476.5; DB 1; Length 679; Best Local Similarity 49.3%; Pred. No. 3.5e-112; Matches 312; Conservative 112; Mismatches 178; Indels 31; Gaps 11;	CE: Murine RCE: talin	: TRE: amino acid : STRANDEDNESS: single : TOPOLOGY: linear : MOLECULE TYPE: protein : HYPOTHETICAL: NO	11 11 11	ROTECTATION INFELLEY 1. RECISTRATION NUMBER: 32.680 TELECOMMUNICATION INFORMATION: TELECHNOE: 202-883-7451 FELERAY. 202-883-7451		.; ORBERTARE: PATENTIA RELEASE #1.0, VECSION #1.25 GURRENT APPLICATION DATA: .; APPLICATION THERE: 115.04.234.583		COUNTRY: US COUNTRY: US IT: 20004 COLUMNS DEPOSIT FORM.) SYKERY: 1499 PANNSYIVANIA AVE, NW ; CITY: Washington ; CTATE: NO	ESS:	APPLICANT: Perchas Smith, Olivia APPLICANT: Wadhwa, Renu APPLICANT: Wadhwa, Renu TITLE OF INVENTION: MORTALIN AND METHODS FOR DETERMINING TITLE OF INVENTION: CONSTRUCTION FOR DETERMINING	US-08-214-583-2 US-08-214-583-2 ; Sequence 2, Application US/08214583 ; Patent No. 5627039 ; Patent No. 5627039	Db 634 HPITOKLYSBÖAG 646	Db 574 AYSLKGOFDDDRQIGGKVDPEDKQAYLDAYEDVAEWLEIHGEDASKEEFEDQRQKLDAYY 633 OY 604 NPIISGIY-QGAG 615	Db 514 TVSAVDKSGKGKPEKLVIKNOKGRLSSEDIEBWYKEAREFAREDXIIKERIEARNTLENV 573 Oy 546 AFNAKAV-EDEGLKKKISEADKKYLDKGGEVISHDAN-TLAEKDEFEKKEKELDOG 603 11 11 11 11 11 11 11 11 11 11 11 11 11	487 NVTATDKS-TGKANKITITNDKGRLSKEELERMVQEAEKYKAEDEVQRERVSAKNALESY	OY 427 IFTTYSDNOPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPHGVPQIEVTEDIDANGIL 486
ATION ANK S ANK S 31 MBER:	APPLICATION NUMBER: US/08/441.139 PILING DARE: 15-MAY-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US 08/080 097	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compartible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Ratentin Release #1.0, Version #1.25 CURRENT AFPLICATION DATA:	CLIF: GATGEN CITY STATE: NY COUNTRY: USA COUNTRY: USA ZIE: 11530 COMPUTER RADABLE FORM:	ONDENCE ADDRESSEE: SCULLY.	APPLICANT: WILITHY DE REI D. APPLICANT: ROCHISON, ANDE S. TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OR SOUTENOSS. 20	Ž 35	RESULT 11	Db 636 AASSIQOASIKLFEMAYKKMASEREGSGSSGTG 668	579 VEAVNMAEGIIHDTETKMEEEKDQLPADECNKL	Qy 536 VSAKNALESYAFNMKSAVEDEGLKGKISEADK-KKVLDKCQEVISWLDANTLAEKDEFEH 594	OY 476 YPPDIDANGILNYJATDKSTGKANKITITUDKGRLSKERIERNYOEAEKYKAEDEVQRER 535 Db 520 YPPDIDANGILNYJATDKSTGKANKITITUDKGRLSKERIERNYOEAEKYKAEDEVQRER 535 Db 520 YPPDIDANGILVYJAKKGGGEOGIVI-OSSGGJSKODEENYKAKEKEEDERKKER 578	OY 416 RNSTIPTKOTOIFTTYSDNOPGYLIGYYEGERAMTKDNYLLGRFELSGIPPAPRGYPOIE 475 : : : : : : : :	OY 356 GRDLNKSINPDEAVAKGAAVQAAILMGDKSENVQDLILLDVAPLSLGLETAGGVMTALIK 415 : :: :	OY 296 SITRARFEBLCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIFKVQKLLQDFFN 355 11 1 1 1 1 1 1 1 1 1	Qy 240 HFYBERKHIKKDISONKRANRELRANDERAKRILSSSTOASLIDISLEEGIDFYT 295	QY 180 ATAYGLDRYGGGENYLLFDLGGGTFDVSILT/IDDGIEFYKATAGOTHLGGSDFDNILYN 239 QY 180 ATAYGLDRYGGENYLLFDLGGGTFDVSILT/IDDGIEFYKATAGOTHLGGSDFDNILYN 239 DD 227 ALAYGLDKSEDKVIAVIDLGGGTFDISILEIQKGVFEVKSTNGDTELGGBDFDQALLR 284	167	Db 112 NPNNTEYATKRIIGRRYDDFEVQKDTKNVPFKIVRASNGDAMVEAHGKLYSPSQI 166 Oy 120 SSMYLTKMKEIABAYLGYPVTNAVITVPAYFNDSGRQATKDAGYIAGLKVLRIINEFTAA 179

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INFORMATION FOR EQU ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
TYPE: amino acids
                                                                                                                      Sequence 5, Application US/09066047A Patent No. 6306394 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 44.1%; Score 1438; DB 1;
Best Local Similarity 46.3%; Pred. No. 4.5e-109;
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TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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                                                                                                                                                                                                                                                                                                                     536
                                                                                                                                                                                                                                                                            577 VISWLDANTLA-EKDEFEHKRKELEQVCNPIISGLY--QGAGGPGPGGFGAQGPKG 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 GGFILSKMRETASTYLGKDVKNAVVTVPAYFNDSQRQATKAAGAIAGLNVLRVVNEPTAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 NPENTFFATKRLIGRRFKEPEVQRDIKEVPYKIVEHSNGD---AWLEARGKT--YSPSQI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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  NUMBER OF SEQUENCES:
                                    TITLE OF
                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                DMARKEAIENGNRAESVCTDIESNLDIHKDKLDQQAVED--LRSKITD-----LRE
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                                                                                                                                                                                                                                                                                                                                                  DEVQRERVSAKNALESYAFNMKS------AVEDEGLKGKISEADKKKVLDKCQE 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFTRLINRNTTIPTRKSQVFSTAADGQTAVEIRVFQGERELVRDNKLIGNFQLTGIAPAP
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                                                                                                                                                                                                                                                                                                                                                                                    KGQPQIEVSFDVDADGIINVSARDKATNKDSSITVAGSSG-LTDSEIEAMVADAEKYRAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVI--NDGDKPKVQVSYKGETKAFYPEEI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ITRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQK 348
                                 COUGHLIN, Richard T.
INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS
                                                                                  MURPHY, Cheryl
STOREY, James
                                                                   BELTZ, Gerald A.
                   USE OF GRANULOCYTIC ERHLICHIA
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US-09-066-047-5
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Best Local
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SEQUENCE CHARACTERISTICS:
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472 PQIEVTEDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEV 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                             PLIERNTTIPTKKSQVFSTAEDGQTAVTIKVYQGERKMAIDNKLLGQFSLEGIPHAPRGV
                                                                                               ALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGV 471
                                                                                                                                                   DFF-GKEPCQGVNPDEVVAVGAAIQGGILTGD----VRDVLLLDVAPLSLGIETLGGVFT 407
                                                                                                                                                                                                 DFFNGRDLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMT 411
                                                                                                                                                                                                                                                                                  FYTSITRARFEELCSDLFRSTLEPVEKALRDAKL-DKAQIHDLVLVGGSTRIPKVQKLLQ 351
                                                                                                                                                                                                                                                                                                                                                     EHMMESFQKETGINLRNDPMAVQRVKEAAEKAK--IELSTRLETDITLPFISSDSTGAKH 292
                                                                                                                                                                                                                                                                                                                                                                                     NHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGID----- 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AALAYGLDK-GDKQRTIVVYDLGGGTFDVSVLEIADGVFEVKATNGDTKLGGEDFDNAIM 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGAFVLEKIKETAERYFGAPVKKAVITVPAYFNDAQRQATKDAGTIAGLDVVRIINEPTA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAAERTIGIDLGTTNSCVAVMEAGTAKVIENSEGSRTTPSVVAFTDNERLVGELAKROAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 649 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/044,869 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-Apr-1998
CLASSIFICATION: <Unknown>
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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STATE: Massachusetts
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48.0%; Pred. No. 7.3e-109;
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US-09-134-001C-3646
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LENGTH: 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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TITLE OF INVENTION: NOLIZEC ACID NAID MAINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NULLECT ACID NAID MAINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE REPERINCE: CTC.007 LEBRADIS FOR DIAGNOSTICS AND THERAPPUTICS
UNREWN PPLICATION WANBER: US/09/134,001C
UNREWN PILING DATE: 1997-08-13
PRIOR APPLICATION WANBER: US/09/044,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                            283
                                                                                                                                                                                                                                                                                                                     303
                                                                                                                                                                                                                                                                                                                                                             223 KENGVDLSQDKMALQRLKDAAEKAKKDLSGVSQTQISLPFISAGENGPLHLEISLTRSKF
                                                                                                                                                                                                                                                                                                                                                                                                            247
                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 LKSTAENYLGDTVDKAVITVPAYFNDGERQATKDAGKIAGLEVERIINEPTAAALAYGLD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 IGIDLGTTYSCYGYFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         march 42.8%; Score 1397.5; DB 4 Local Similarity 47.4%; Pred. No. 8.6e-106; les 303; Conservative 113; Mismatches 174.
                                                                                                                                                                                                    INPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKETAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGYTAGLNYLRIINEPTAAAIAYGLD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLQQKYDALMNLSMKLGEAAYAANKNDGAGSADQSGSSSGGSDGNPEERVVD 634
NGIVNVTAKDLGTNKEQNITIQSSSS-LSDEEIDRMVKDAEENAEADKKRREEVDLRNEA 516
                                        NGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNAL 542
                                                                                       SKSQVYSTAADNQPAVDIHVLQGERPMASDNKTLGRFQLTDIPPAPRGVPQIEVTFDIDK 457
                                                                                                                                KQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDIDA 482
                                                                                                                                                                              VNPDEVVAMGAAIQAGVITGD----VKDVVLLDVTPLSLGIEIMGGRMNTLIERNTTIPT
                                                                                                                                                                                                                                                                                                                  EELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKS 362
                                                                                                                                                                                                                                                                                                                                                                                                         RKHKKDISQNKRAVRRLRTACERAKRTLS--SSTQASLEIDSLFEG--IDFYTSITRARF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KT-ETDQKVLVFDLGGGTFDVSILELGDGVFEVLSTAGDNKLGGDDFDQVIIDYLVSEFK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQSIKRHMGTDY-------KVDI----EGKSYTPQELSAMILQN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFEHKRKELEQVCNPIISGLYQGAGGPGPGGPGAQG-PKGGSGSGPTIEEVD 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRERVSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWL-DANTLAEKD 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113; Mismatches 174;
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184

186 DRTGKGERNVLIEDLGGGTEDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEF 245

DKKGK-EEHVLIFDLGGGTFDVSLLFIEDGIFEVKATAGDTHLGGEDFDNRLVNHFIQEF

124 KMKETAESYLGAKVNDAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAAIAYGL

183

KMKEIABAYLGYPYTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGL 185

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US-08-928-692-52
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                                                                                                                                     ; MOLECULE TYPE: No. 5958727e
US-08-928-692-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52, Application US/08928692 Patent No. 5958727
                                                                   Matches 264;
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASLSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lamsa, Michael APPLICANT: Hansen, Kim TITLE OF INVENTION: Methor TITLE OF INVENTION: a POIL NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                       NAME: Lambiris, Elias J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 ESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQV 602
                                                                                 Local Similarity
                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 12-SEP
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/928,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 405 Let
CITY: New York
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                                                                                                                                                                                                                       LENGTH:
4 AVGIDLGTTYSCVAHFANDRVDIIANDQGNRTTPSFVAFTDTERLIGDAAKNQAAMNPSN 63
                     6 AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQN 65
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                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a Polypeptide
                                                                                 41.5%; Score 1354; DB 2;
78.1%; Pred. No. 1.2e-102;
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                                                                                                                                                                                                                                                                                                                                  33,728
                                                                                                                                                                                                                                                        52:
                                                                 37; Mismatches
                                                                                                                                                                                                                                                                                                                         4944.200-US
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                                                                                                  Length 339;
                                                                   Indels
                                                                 2,
                                                                 Gaps
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LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
YOULGULE TYPE: NO. 6323002e
US-09-339-972-52
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US-09-339-972-52
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Best Local S
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Patent No. 6
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SED ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Brody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: ...
NAME: Lambiris, Elias J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Methods for Modifying the Production TITLE OF INVENTION: a Polypeptide
124
                                 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 CSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRI 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 KRKNKKDLSTNGRALRRLRTACE-SQENFVSSAQTSVEIDSKNEGIDFYTSITRARFEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
                                                                                                                                                                                                          Local Similarity
hes 264; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                   64 TVFDAKRLIGRNENDPEVQADMKHFPFKLIDVDGKPQIQVEFKGETKNETPEQISSMYLG
                                                                                                     66 TVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/339,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                       6 AIGIDLGTTYSCYGYFQHGKYEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQN 65
KMKETAESYLGAKVNDAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAAIAYGL
                               KMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEEL
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6323002
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405 Lexington Avenue
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                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                          41.5%; Score 1354; DB 4; 78.1%; Pred. No. 1.2e-102; tive 37; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
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                                                                                                                                                                                                        37; Mismatches
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                                                                                                                                                                                                                                          Length 339;
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Search completed: December 4, 2002, 16:43:52 Job time : 18 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      3136
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Gapop 10.0 , Gapext 0.5
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          SPTREMBL_21:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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          Q9QWJ5
Q925V6
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78.7	79.1	80.3	80.7	81.7	82.5	82.5	82.5	83.2	83.4	83.6	83.7	84.0	84.1	84.2	84.3	84.3	84.4	84.4	84.5	84.5	84.5	84.5	84.5	84.5	84.7	84.7	85.1	85.1
586	566	645	663	646	665	644	646	643	656	651	640	644	653	645	643	639	645	645	653	650	647	637	636	658	633	638	659	649
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Q961s6 homo sapien	3	4		001948 trichinella	Q24789 echinococcu	Q95v47 artemia san	Q94614 mesocestoid	Q8uuj8 brachydanio		Q8sxq4 drosophila		parastrong	Q17310 ceratitis c			0		O96541 setaria dig		5			Q9tug3 capra hircu	Q27121 urechis cau			Q9xzj2 crassostrea	P79984 brachydanio

ALIGNMENTS

WANS9 PRELIMINARY; PRT; 640 AA. GRWAS9. OHMAR-2002 (TrEMBLICE). 20, Created) OHMAR-2002 (TrEMBLICE). 20, Last sequence update) Heat Shock protein 70. Heat Shock protein 70. Ekstyota; Sections; Chordata; Craniata; Vertebrata; Eutelcostomi; Entheria; Carnivora; Flasipedia; Canidae; Canis. Ekstyota; Sections; Carnivora; Flasipedia; Canidae; Canis. ADe K. Kano R., Hasegawa A.; Canine heat Shock protein 70 (hap70) mRNA, complete ods.*; SEQUENCE FROM N.A. ADe K. Kano R., Hasegawa A.; Canine heat Shock protein 70 (hap70) mRNA, complete ods.*; SEDDIENCE FROM N.A. ADE K. Kano R., Hasegawa A.; Canine heat Shock protein 70 (hap70) mRNA, complete ods.*; SEDDIENCE FROM N.A. Exst. Fasipora; SEDDIENCE FROM N.A. SEDOISTE; PROJO13; HSP70; 1 (hap70) mRNA, complete ods.*; SEDDIENCE FROM N.A. SEOUENCE 640 AA: 69935 MM; 402F3E91871BFBFF CRC64; WASCANCIDLGTTYSCVOVPODIGNETIANDGONETPSVAFTDTERLICODAKKNOVA 1 1 MAKSANCIDLGTTYSCVOVPODIGNETIANDGONETPSVAFTDTERLICODAKKNOVA 1 1 MAKSANCIDLGTTYSCVOVPODIGNETIANDGONETPSVAFTDTERLICODAKNOVA 1 1 MAKSANCIDLGTTYSCVOVPODIGNETIANDGONETPSVAFTDTERLICODAKNOVA 1	ОУ	ap dy	Query Ma Best Loc Matches	SQ SE							RL Su									_	DE He	DT 01			Q8WNS9
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PRT: 640 AA. , Created) , Last sequence update) , Last annotation update) , Last annotation update) 70 (hsp70) mRNA, complete ods.*, 170 (hs	AKRLIGRKFGDE AKRLIGRKFGDE	DLGTTYSCVGVE	98.28 nrity 98.38 nnservative	AA: 69935	129; HSP70_2;	97; HSP70_1;	1; HEATSHOCK	HSP70; 1.	01023; Hs p70	; BAB78505.1	r-2001) to th	hock protein	l., Hasegawa	N.A.		5	eria; Carniv	.azoa; Chorda	is (Dog).		tein 70.	•			ET.TMTNARY:
tation update) tation update) tation update) a; vertebrata; Eutcleos edia; Canidae; Canis. edia; Canidae; Canis. ank/DDBJ databases. ank/DDBJ databases. 1018718887F CRC64; 2.1e174; 1118111111111111111111111111111111111	PVVQSDMKHWPF 	FQHGKVEIIAND	s; Score 32 s; Pred. No 5; Misma	MW; 402F3E	UNKNOWN_1.	UNKNOWN_1.	K70.				ne EMBL/GenB	n 70 (hsp70)	A.;				ora; Fissip	ata; Craniat					Last		
e) e; Canis. e; Canis. e; Canis. hbases. abases. abases. alphases. lililililidha rupteriigha	QVINDGDKPKVQ : QVVNDGDKPKVQ	QGNRTTPSIVAF QGNRTTPSIVAF	03.5; DB 6; 2.1e-174; tches 5;	91871BF87F C							ank/DDBJ dat	mRNA, compl					edia; Canida	a; Vertebrat				tation updat	ence update)		640 AA
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Query Match
                          PROSITE; PSULVACATE binding.
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Q9QWJ5;
01-MAY-2000
01-MAY-2000
01-MAR-2002
                                                                                                                                                              Rowen L. Madan A., Qin S., Hall J., Dahl T., James R.,
Schaffer T., Batcliffe A., Abbasi N., Lorett C., Lasky.
Schaffer T. Batcliffe A., Abbasi N., Lorett C., Lasky.
Schaffer Of the mouse MHC class TII region. ",
"Sequence (MVY-1998) to the EMBLOGENBANK, DDBJ databases
submitted (MVY-1998) to the EMBLOGENBANK DDBJ databases
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAN
                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
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                                                  PRINTS; PR00301; HEATSHOCK70.
PRODOM; PD000099; HSp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                           InterPro; IPR001023; Hsp70. Pfam; PF00012; Hsp70; 1.
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HSSP; P08107; 1HJO.
MGD; MGI:105975; H2-Bf.
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         Score
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0925V6;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                          Mus musculus
                                                                                                                                  HSP70
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 pfam; PF00012; HSP70; 1.
proDom; PD000089; HSP70; 1
pROSITE; PS00297; HSP70_1;
                                                                                                  NCBI_TaxID=10090;
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LNPONTYFDAKRIJGKFGDAVVQSDMKHMPFQVINGGKFKVQVSVGSTKAFYEREIS 120

LNPONTYFDAKRIJGKKFGDAVVQSDMKHMPFQVVNDGDKFKVQVNYKGESRSFFPEEIS 120
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                                                                                                                                        (TrEMBLrel.
L (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                        PRELIMINARY;
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                                                                                                           ; Chordata; Rodentia;
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0; Mismatches 10;
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Sciurognathi; Muridae; Murinae; Mus
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annotation
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SEQUENCE PROM N.A.
STRAIN-MISTRAE, TISSUE-SPLEEN:
MEDLINE-94190258, PubMed-8141767;
Meetril R., Chi S.H., Sayon M.R., Dillmann W.H.
*Isolation of a novel inducible rat heat shock
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                                                                                                                          SMYLTKMKETAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA
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610; Conser
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Pred. No. 2.6e
14; Mismatches
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Query Match
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Matches 572; Conserv
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PRIMIS PR00011; HEAVEROCK70.
PRODOM: PR0000099; H8970; 1.
PR0SITE: P8000297; H8970; 1.1
PR0SITE: P800029; H8970; 2.1
PR0SITE: P801039; H8970; 3.1
PR0SITE: P801039; H8970; 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-98351992; PubMed-9685725;
Ito Y. Ando A., Ando H., Ando J., Saijoh Y., Inoko H., Fujimoto
"Genomic Structure of the spermatid-specific HSP70 homolog gene
boated in the class III region of the major histocompatibility
complex of mouse and man.";
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                         LESYAPINMKSAVEDEGLKGKISEADKKKVLDKCQEVISMLDANTLAEKDEFEHKRKELEQ
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641 AA
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                  GCTGPACGTGYMPGRPATGPTIEEVD
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Pred. No. 1.5e-158
34; Mismatches 25
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Matches 572
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Q960C9
01-DEC-2001 (Tremblrel. 1
01-DEC-2001 (Tremblrel. 1
01-Mar-2002 (Tremblrel. 2
Heat shock protein.
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PROSITE; PSO
ATP-binding.
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"Homo saptens 2.29 MIJbp genomic DNA of 5p21.3 HLA class I region.";
Submitred (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-1 SIMILARITY: BELOWS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
BMBL, AP000503; Ha663301.1;
Interpression 198001033; Hsp70...
Interpression 198001033; Hsp70...
Interpression 198001033; Hsp70...
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PROSITE: PS00299; HsP70_1; UNKNOWN_1.
PROSITE: PS00329; HsP70_2; UNKNOWN_1.
PROSITE: PS01036; HSP70_3; UNKNOWN_1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirakawa M., Yamaguchi H., Imai K., Shimada J. Submitted (SEP-1999) to the EMBL/GenBank/DDBJ
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                                                        TKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFDLTGIPPAPRGVPQIEVTFDID
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ANGILNVTAMDKSTGKVNKITITNDKGRLSKEEIERMVLDAEKYKAEDEVQREKIAAKNA
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; Pred. No. 1.56
34; Mismatches
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Best Loc
Matches
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PRODOMM, PRO000089; HEAPTO. 1.
PROSITE: PS00229; HEAPTO. 1. 1.
PROSITE: PS00229; HEAPTO. 2; 1.
PROSITE: PS00239; HESPTO. 3; 1.
ATP-binding; Heat shock.
SEQUENCE GAI AA; 706.33 MM;
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01-WOV-1998 (TrEMBLrel. 08, Created)
01-WOV-1998 (TrEMBLrel. 08, Last sequence up
01-WAR-2002 (TrEMBLrel. 20, Last annotation
Spermatid specific heat shock protein 70,
HSFAIL OR HSC/OT.
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InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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-:- SINILARITY: BELONGS TO THE
EMBL; D85732; BAA32522.1; -.
HSSP; P08107; 1HJO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ito Y., Ando A., Ando H., Ando J., Saijoh Y., Genomic structure of the spermatid specific located in the class III region of the major complex of mouse and man.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/C: TISSUE-TESTIS;
MEDLINE=98351992; PubMed=9685725;
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89.0%; Pred. No. 1
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2; Mismatches 36;
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Sciurognathi; Muridae;
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PRINTS: PR00013; HSATSHOCKYO.

PRODOM: PD000089; HSP70; 1.

PROSITE: PS00029; HSP70_1; UNKNOWN_1.

PROSITE: PS01036; HSP70_2; UNKNOWN_1.

SEQUENCE 651 AA; 71055 MW; BCC75F)
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Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Caudata;
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Ordonez M.R., Pichon L.L., Laurens V
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Pred: No. 4.6e-153;
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Salamandroidea; Ambystomatidae;
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01-NG-1998 (TEMBLrel. 07, Created)
01-NG-1998 (TEMBLrel. 07, Last sequence up
01-NAR-2002 (TEMBLrel. 20, Last annotation
Heat shock cognate 70 kDa protein.
HSC70.
Gallus gallus (Chicken).
                                                   Pfam; PF00012; HSP70, 1.

PRINTS; PR00301; HSP70, 1.

PROSITE; PS00309; HSP70, 1.

PROSITE; PS00297; HSP70, 2; 1.

PROSITE; PS01030; HSP70, 2; 1.

PROSITE; PS01030; HSP70, 2; 1.

PROSITE; PS01030; HSP70, 3; 1.
   SEQUENCE
                                                                                                                                                                                                                                                                   -1- PTM: METHYLATED (TRI-) ON LYSINE ON ARGININE RESIDUE(8).
-1- SINILARITY: BELONGS TO THE HEAT SEMBL; AJ004940; CAA06233.1; -.
                                                                                                                                                                                                                                                                                                                                                         by virus transformation."; Arch. Biochem. Biophys. 297:169-175(1992)
                                                                                                                                                                                                                                                                                                                                                                                          alterations by arsenite treatment, by virus transformation.":
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Best Local
Martial J.A., Muller M.;
"Cloning and expression an
tilapia fish.";
FEBS Lett. 474.5-10(2000)
-!- SIMILARITY: BELONGS TO
                                                                                                                                                                                073922;
073922;
01-AUG-1998
01-AUG-1998
01-MAR-2002
                                                                                                                 Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica). Eukaryota; Metazoa; Chordata; Cranlata; Vertebrzata; Euteleostomi; Actinopterygii, Neopterygii, Teleostei; Euteleostei; Meoteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroide
                                                   MEDLINE=20291068; PubMed=10828441; Molina A., Biemar F., Mueller F.,
                                                                                            Cichlidae; Oreochromis.
NCBI_TaxID=8127;
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SEQUENCE 639 AA;
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PRODOM; PD000089; HSP70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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Pfam; PF00012; HSP70; 1.
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85.8%; Pred. No. 1.4
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Euteleostei; Neoteleostel;
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TONA Cloning of Hear-inducible HEP70, a 70.6 ki

In Japanese Flounder Paralichtys Olivaceus.*;

Fisheries Sci. 0:0-01999;

--- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEI

RESE: A0010871: NA31697.1;

HESF: P00107, 1HJO.
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Best Local S
Matches 539
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Pfam: PF00012; HSP70; 1.
Probom: P0000089; HSP70; 1.
PR0SITE: PS0029; HSP70, 1.
PR0SITE: PS0029; HSP70, 2.
PR0SITE: PS01036; HSP70, 3; 1.
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NCBI_TaxID-9255;
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FEELNSDLERGTLEPVEKALRDAKLDKSKIHEIVLYGGSTRIPKIQKFLQDFFNGRELIK
FEELNSDLERGTLEPVEKALQDSKHDKSKIHEIVLYGGSTRIPKIQKFLQDFFNGRELIK
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                                                          LESYAPNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQ
                                                                                                        ANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNA
                                                                                                                                         TKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELAGIPPAPRGVPQVEVTFDID
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539; Conserv
                      VCNPIISGLYOGAGGPGPGGFGAOGPKGGSGSGPTIEEVD
                                             LESYVYHMKSSVEDDSMKGKIQEEDKKIVIDKCNQTISWLENNQLAEKDEYEHQQKELEK
                                                                                           ANGILNVSAVDKSTGKENKITITNDKGRLSKQEIEQMVQDAEKYKADDELKRDTITARNS
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; HSP70_3; 1.
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;; Pred. No. 1.9e
59; Mismatches
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70, a 70.6 kDa Heat Shock
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PRELIMINARY;

PRT;

639

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Query Ma
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Matches
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Pfam: PF00012; HSP70; 1:
PRINTS: PF000301; HEATSHOCK70.
PF000089; HSP70; 1:
UNKNOWN_1.
PR0SITE; PS00297; HSP70_1; UNKNOWN_1.
PR0SITE; PS00239; HSP70_2; UNKNOWN_1.
SEQUENCE 639 AA; 70128 MM; 87382F
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Q8UWM9;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
Stress prote
HSP70-2.
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EMkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthonorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2001) to the EMBL; AB062114; BAB72168.1; InterPro; IPR001023; Hsp70.
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      VCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
                                                   LESYAPNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQ
                                                                                                         ANGILNYTATDKSTGKANKITITNDKGRLSKEEIERMYQEAEKYKAEDEYQRERYSAKNA
                                                                                                                                                                      TKQTQIFTTYSDNQPGVLIQVYEGERANTKDNNLLGRFELSGIPPAPRGVPQIEVTFDID
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                                                                                           ANGILNVSAVDKSTGKENKĪTĪANDKGRLSKDEIERMVQDAEKYKAEDELQRDKIAAKNS
                                                                                                                                                     TKQTQVFSTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELTGIPPAPRGVPQIEVTFDVD
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R-2002 (TrEMBLrel. 20, 1
N-2002 (TrEMBLrel. 21, 1
S protein HSP70-2.
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539; Conser
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84.2%; Pred. No. 2
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Last annotation update)
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Best Local Similarity 83.4
Matches 542; Conservative
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01-AUG-1998 (TrEMBLTel. (
01-NOV-1998 (TrEMBLTel. (
01-MAR-2002 (TrEMBLTel. )
Heat shock protein 70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO
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Kim W.J., Lee J.H., Kim K.K., Lee S.J., Kang H.S., Kim H.D.;

"Molecular cloning and characterization of a heat shock protein
related CDMA from olive flounder (Paralichthys olivaceus).";

Han-gug Yangsig Hag-heej 12:91-100(1999).

1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

EMBL, RF055099, AAC33859.1; ...

EMBL, RF055099, AAC33859.1; ...

TASSP, P19120, 1ATR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0301; HEATSHOCK70.
PRODOM; PRO00089; HSP70; 1.
PROSITE; PS00237; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paralichthys olivaceus (Flounder).

Bukaryota: Metazoa: Chordsta: Craniata: Vertebrata: Buteleostomi;
Actinopterygii; Macpterygii; Teleostei; Buteleostei; Naoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectidei; Paralichthyidae; Paralichthys.

Pleuronectidei; Paralichthyidae; Paralichthys.
    421
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Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                              PTKQTQTFTTYSDNQPGVLIQVYEGERAMTRDNNLLGKFELTGIPLAPRGVPQIEVTFDI
                                                            KSINSDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI
                                                                          KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                                      RFEELNADLFRGTLDPVEKSLRDAKMDKGQIHDIVLVGGSTRIPKIQKLLQDFFNGKELN
                                                                                                                                        RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                                                                                                                 FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
                                                                                                                                                                                                                                                         IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
                                                                                                                                                                                                                                                                                                  SMYLTKMKETAEAYLGKTVNNAVYTVPAYFNDSQRQATKDAGTISGLNYLRIINEPTAAA
                                                                                                                                                                                                                                                                                                                 SMYLTKMKEIAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGYIAGLNYLRIINEPTAAA 180
                                                                                                                                                                                                                                                                                                                                                          MNPTNTVFDAKRLIGRRFDDAVVQSDMKHWPFNVINDSTRPKVQVEYKGESKSFYPEEIS
                                                                                                                                                                                                                                                                                                                                                                           LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
                                                                                                                                                                                                                                                                                                                                                                                                                    MSKGPAVGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDSERLIGDAAKNQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                     MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
                                                                                                                                                                                                                                        IAYGLDKKYGSERNYLILDLGGGTFDYSILTIEDGIFEYKSTAGDTHLGGEDFDNRMYNH
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Pred. No. 5.5e
49; Mismatches
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Best Loc
Matches
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PROSITE: PS01036; HSI
PROSITE: PS01036; HSI
ATP-binding.
655 AA;
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Q919Q5;
Q1-OCT-2000
Q1-OCT-2000
Q1-MAR-2002
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Eukaryota: Metazoas (chordata; Cranata; Vertebrata; Euteleostoni;
Eukaryota; Meopterygii; Poloostai; Euteleostei; Meotaleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Aplocheilidae; Rivulinae; Rivulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00301; HEATSHOCK70
PRODOM; PD000089; Hsp70; 1.
PROSITE; PS00297; HSP70_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identification of a novel muscle-preferred regulatory element.",
Nucleic Acids Res. 29:3041-3050(2001).
-1- SIMILARITY: BELOWGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, RP227986; AAF71255.1; -.
HSSP; D0B109, LCKR.
InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-21345298; PubMed-11452029; MEDIINE-21345298; Young S., Lee J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00012; HSP70;
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Rivulus marmoratus and analysis of its expression in skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim C.G.;
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FIAEFKRKFKKDIVSNKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGTDFYTSITRA
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546; Conserv
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HSP70_2; 1.

HSP70_3; 1.
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pred. No. 5.9e-151;
figure 151;
figure 151
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Matches 544; Conserv
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Rauch G.J., Klein J.;
"Conservation of mho class III region
human as determined by radiation hybri
J. Immunol. 165:6984-6993(2000).
                                                                                                                                                                                                                                                        Suelimann H., Murray B.W., Klein J:
"Analysis of Ancient Mhc Class III Synteny by Mapping of Orthologous Genes in the Zebrgfish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
                                                                                                                      PRODOM: PD000089; Hsp70; 1.
PROSITE: PS00297; HSP70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
PROSITE: PS01036; HSP70_3; 1.
                                                                                                                                                                                                          Submitted (DEC-1999) to the RMBL/GenBank/DDBJ databases -- SIMILATIT: BELONGS TO THE HEAT SHOCK PROTEIN 70 FA EMBL, AF210640; AAF70445.1; -- HSSP; P08109; 1CKR.
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PRINTS; PR00301; HEATSHOCK70.
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Pfam; PF00012; HSP70; 1.
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A., Murray B.W.,
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Copyright (c) 1993 - 2002 Compugen Ltd
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76.7	77.0	77.0	77.1	77.2	77.4	77.5	77.5	78.2	78.5	78.6	80.1	81.5	81.6	81.8	83.2
649	651	651	644	651	647	651	651	647	645	640	637	640	641	654	651
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S53126	S46302	T48271	S67431	S03250	T41121	T45517	JC4786	T45522	JC5642	T43730	A48469	HHKW7A	JN0668	S27004	A36333
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ALIGNMENTS

Фр	Qу	Qy Db	ОУ	Фу	оу рь	Оу	Que Bes Mat	ARSULT ARS971 dnak-t-t N+Alte C;Space C;Space C;Acce R;Min Immuno
361 KSINPDENVAYGAAVQAATIAGDKSERVQDLLLLDVAPLSCLEFAGGEVPTALTKRNSTI 420 361 KSINPDEAVAYGAAVQAATIAGDKSERVQDLLLLDVAPLSLGLEFAGGEVPTALTKRNSTI 420	301 RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN 360 	241 PVEETKRHKKDISQNKRAVERLETACERAKETLSSSTOASLEIDSLEFEGIDFYTSITRA 300 241 FVEETKRHKKDISQNKRAVERLETACERAKETLSSSTOASLEIDSLEFEGIDFYTSITRA 300 241 FVEETKRHKKDISQNKRAVERLETACERAKETLSSSTOASLEIDSLEFEGIDFYTSITRA 300	181 TAYGLDRIGKGERNYLIPDLGGGTPDVSILTIDDGIFBVKATAGDTHLGGEDEDNRLYNH 240 	121 SAVLTKAKETAEN LEYPYTANNITTVAN PROSEROATKOACYTAGLAVLEI INEPTAAA 180 121 SAVLTKAKETAEN TURTUTTURAY PROSEROATKOACYTAGLAVLEI INEPTAAA 180 121 SAVLTKAKETAEN TUGYPYTANNITVAN PROSEROATKOACYTAGLAVLRITAEN PAAA 180	61 LNPONTVEDAKRIJGRKEGDEVYQSDMKHHPFQYINGDKPKYQVSYKGETKAFYEEIS 120 	1 MAKAAAIGIDLGTTYSCUGVPQHGKUEILANDGONRTTESYVAFTDTERLIGDAAKNUVA 60 	Query Match 100.0%; Score 3263; DB 2; Length 641; Best Local Similarity 100.0%; Pred. No. 2e-172; Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 1 A45871 dnak type molecular chaperone HSP70-1 - human MyAlternate names: heat shock protein HSP70-1 C.Species: Heno saplens (man) C.Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 20-Aug-1999 C.Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 20-Aug-1999 C.Date: 03-Mar-1994 #sequence_revision 05-Mar-1994 #text_change 20-Aug-1999 C.Accession: A45871 A.Tille: Structure and expression of the three HHC-linked HSP70 genes. A.Tille: Structure and expression of the three HHC-linked HSP70 genes. A.Tille: Structure and expression of the three hHC-linked HSP70 genes. A.Tille: Structure and expression of the three hHC-linked HSP70 genes. A.Tille: A45871 A.Tille: A45871 A.Roccussion: A45871 A.Stock=references: GB:M59828; GB:M34267; NID:g188487; PIDN:AAA63226.1; PID:g188488; C.Function: Involved in protein folding and assembling/disassembling of protein co. Superfemily: heat shock protein 70 C.Superfemily: heat shock protein folding C.Superfemily: heat shock protein folding C.Superfemily: heat shock protein folding

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A;Map position: 6p21.3-6p21.3
A;Introns: #status absent
C;Function:
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Nucleic Acids Res. 14, 8933-8948, 1946
A.Title; In vitro transcription of a human
A;Reference number: I3756; MUID:87066768;
A;Accession: I37561
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A.Mote: the authors mistranslated residues 463, 491, and 492
R:Drabent, B.; Genthe, A.; Benecke, B.J.
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Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985

Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985

A:Title: Conserved features of eukaryotic hsp70 genes revealed A:Reference number: A29160; MUID:86016721; PMID:3931075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Homo sapiens (man)
C:Date: 16-Aug-1988 #sequence_revision 02-Jul-1996
C:Accession: A93160; I:17561; I:37562
R:Hunt, C.; Morimoto, R.I.
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C;Genetics:
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A; Residues: 616-640 < RE2>
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A; Status: translation not shown;
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A; Residues: 1-22 < RES>
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N;Alternate names: heat shock protein,
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SMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA
                  SMYLTKMKETAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA 180
                                                                    LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
                                                                                                     LNPQNTVFDAKRLIGKKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPERIS
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Pred. No. 2.7
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PMID:3786141
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RESULT 3
S53357
dnaK-type molecular chaperone hsp70 - bovine
N.Alternate names: 70K heat shock protein
C:Species: Boa prindgenius taurus (cattle)
C:Date: 05-Dec-1998 *sequence_revision 05-Dec
C:Accession: S53357
R:Gutterrez, J.A.; Guerriero Jr., V.
R:Gutterrez, J.A.; Guerriero Jr., V. Biochem, J. 305, 197-203, 1995
A.Title: Chemical modifications of a recombinant bovine A.Reference number: \$53357; MUID:95126904; PMID:7826329
A.Recession: \$53357
A.Scause: perilminary A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone C; Function: C; Genetics: A;Cross-references: EMBL:U09861; NID:g497937; A; Molecule type: mRNA A; Residues: 1-641 <GUT> hsp70 bovine 05-Dec-1998 #text_change and PIDN: AAA73914.1; assembling/disassembling stress-inducible PID:g497938 21-Jul-2000 o. 70 protein kDa

heat-

121 121

> SMYLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA LNPQNTVFDAKRLIGRKFGDPVVQSDMKEWPFRVINDGDKPKVQVSYKGETKAFYPEEIS LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDXPKVQVSYKGETKAFYPEEIS MAKNMATGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA

180 120 120 60

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SMYLTKMKEIAEAYLGHPYTNAVITYPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA

61 61 ب

1 MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA

633; Similarity Conservative

98.6%;

Score 3216; DB 2; Pred. No. 7.9e-170; Mismatches

Length Indels

0; Gaps

0

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Immunogenetics 35, 286-289, 1992
A: Mitle: Complete nucleotide sequence of a po-
A: Reference number: S35718; MUID:92175874; PM
A: Accession: S35718
A: Status: translation not shown
A: Moleoule type: DNA
A: Resiluee: type: DNA
A: Resiluee: EMBL: M69100
C: Genetics: Complete Sumble: M69100
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$35718

GHAK-Type molecular chaperone hsp70 - pig

W:Alternate names: heat shock protein hsp70

C;Species: Sus scroia domestics (domestic pig)

C;Species: 99-bec:1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C;Accession: $35718

C;Accession: $35718

A. R.; Van de Weghe, A.R.; Coppleters, W.R.; Van Zeveren, A.J.; BC
                                                                                                                                                                                                                                                                          A;Description: involved
C;Superfamily: heat show
C;Keywords: ATP; molecul
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C;Function:
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                               SMVLTKMKEIAEGYLGHPVSNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA
                                                            SMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA 180
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leat shock protein 70
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A; Molecule type: I
A; Residues: 1-70,
                             A; Reference number: A; Accession: S47522
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                                                                                                                                                                                                                                                                     A;Residues: 1-641 <WAL2>
A;Cross-references: EMBL:X77208;
                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated
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A; Accession: 168
                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: HSP70.1
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A; Residues: 1-641 <WAL1>
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C;Date: 02-Aug-1996 *sequence_revision 02-Aug-1996 *text_change C;Accession: 154342; 168986; 843388; 847522; 158574; S33955; S38 R;Walter, L.; Rauh, F.; Ginther, E. Immunogenetics 40, 325-330, 1994 A.FitLe: Comparative analysis of the three major histocompatibility A.Fetéreance number: I54542; MUID:95012453; PMID:7927536 A;Accession: I54542 N;Alternate names: dnaK-type molecular chaperone HSP701b; heat shock protein C;Species: Rattus norvegicus (Norway rat) from GB/EMBL/DDBJ S38199; 08-Dec-2000 complex-linked S41413; S41414 70

A;Cross-references: EMBL:X77207; NID:g1814000; PIDN:CAA54422.1; PID:g450930

from GB/EMBL/DDBJ

NID:g927512; PIDN:CAA54423.1;

PID:g450932

A;Title: Isolation of a novel inducible rat heat-shock A;Reference number: \$43388; MUID:94190258; PMID:8141767 A;Accession: \$43388 protein (HSP70) gene and

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A;Molecule type: DNA
A;Residues: 1-70,'NG',73-109,'K',111-203,'R',205-261,'P',263,'ADGV',268-641
A;Cross:references: EMDL:X7555'; NID:9407164; PIDN:CAA53140.1; PID:9407164
A;Experimental source: ischaemic rat heart

R;Lisowska, K.; Widlak, W.; Krawczyk, Z.; Wolniczek, P.; Wisniewski, Biochim. Biophys. Acta 1219, 64-72, 1994
A;Title: Clonlug, nucleotide sequence and expression of rat heat ind A;Reference number: S47522; MUID:94368874; PMID:8086479 inducible hsp70

gene

heat shock

prot

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mclecule type: mRNA
A;Residues: 1-226. /br, 228-641 <LON>
A;Cross-references: GB:L15764; NID:g294567; PIDN:AAA17441.1; PID:g294568
A;Cross-references: GB:L15764; NID:g294567; PIDN:AAA17441.1; PID:g294568
C;Cenetics: <4SEP1>
A;Gene: hsp70.1
C;Genetics: <4SEP1>
A;Gene: hsp70.2
C;Function: involved in protein folding and assembling/disassembling
C;Superfamily; heat shock protein 70
C;Superfamily; heat shock protein 70
C;Superfamily; heat shock; molecular chaperone; stress-induced protein
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RESULT 6
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dnaK-type molecular chaperone
dnak-type mames: heat shock
N;Alternate names;
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                                                                                                                                          DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERNVQEAERYKAEDEVQRERVAAKN
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619; Conserva
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Pred. No. 3.1e-167;
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70
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C;Date: 13-Jan-1955 #sequence_revision 13-Jan-1955 #txxt_change 20-Aug-1999
C;Accession: 531766; 156927
R;Sachais, I.; Angelidis, C.; Bota library, January 1993
submitted to the BMBL Data library, January 1993
A;Description: No. 101766 esquence of the CDNA encoding a monkey 70kd heat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Sainis, I., Angelidis, C.; Pegoulatos, G.; Lazaridis, I.
FBBS Lett. 355, 282-286, 1994
A;Title: The hsc/O gene which is slightly induced by heat
A;Teference number: 136927, MUID:95080396; PMID:9988690
A;Reference number: 136927, translated from GB/EMBL/DDBJ
A;Status; preliminary; translated from GB/EMBL/DDBJ
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A.;Residues: 1-638 <RES>
A.;Coss.references: EMBL:X70684; NID:922781; PIDN:CAA50019.1;
A.;Experimental source: kidney; cell line COS-1
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A; Accession: S31766
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                                                                                          FVEEFKRKHKKDISQNKRAVRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
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                                                       QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
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Pred. No. 4.1e-166;
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N;Alternate names: heat shock protein 70
C;Species: Mus mussollus (house mouse)
C;Date: 31-Dec:1990 #sequence_revision 31-Dec:1990 #text_change 20-Aug-1999
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R;Hunt, C.; Calderwood, S.
Gene 87, 192-204, 1990
A;Title: Characterization and sequence of a mouse hsp70 gene A:Reference number: JH0095; MUID:90236310; PMID:2332169
A;Accession: JH0095
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A; Residues: 1-642 <HUN>
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                                                        QVCNPIISGLYQGAGGPGPGGFGAQG-PKGGSGSGPTIEEVD 641
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                                   RVCSPIISGLYQGAGAPGAGGFGAQAPPKGASGSGPTIEEVD
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Pred. No. 7.8
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C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-641 <MIL>
A;Cross-references: GB:M59829;
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. Title: Structure and expression of the three MHC-linked HSP70 A; Reference number: A45871; MUID:91055806; PNID:1700760 A; Accession: B45871
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  molecular chaperone Hsc70t
                                                                                                                    VCNPIISGLYQGAGGPGPGGFGAQGPKGGSG-----SGPTIEEVD 641
                                                                                                                                                     LESYAFNMKSVVSDEGLKGKISESDKNKILDKCNELLSWLEVNQLAEKDEFDHKRKELEQ
                                                                                                                                                                                      LESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQ
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32, 242-251, 1990
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Pred. No. 1.5e-153;
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N.Alternate names: heat shock protein 70
C:Species: Mas musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: 14976;
R:Snoek, M., Olavesen, M.G., van Vugt, H.; Milner, C.M.; Teuscher, C.; Campbell,
A.Title: Coding sequences and levels of expression of Hsc70t are identical in m:
A. Hecternee number: 149761, MUID:94299288; PMID:8026864
A. Accession: 149761
A. House prolliniary; translated from GB/EMBL/DDBJ
A. Molecule type: DMA
A. Molecule type: 
RESULT 10
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dnaK-type molecular chaperone
N;Alternate names: heat shock
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Pred. No. 4.5e-152;
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C:Date: 06.7an.1995 ssequeno
C:Accession: S41415; 168987
R:Lutz, W.
submitted to the EMBL Data I
A:Reference number: $41413
A:Accession: S41413
A:Accession: S41413
A:Accession: S41413
A:Accession: S41413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X77209;
R;Walter, L.; Rauh, F.; Gunther,
Immunogenetics 40, 325-330, 194
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C/Function:
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A; Residues: 1-641 <RES>
A; Cross-references: EMBI
C; Genetics:
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                                  EEPKRKHKOISONKRAYRKLATACEBAKRTLSSSTOASLEIDSLEGGIDFYTSTIRARF
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PONTVEDAKRLIGRKEGEPVVGSDMKLMPFQVINDAGKFKVGVSYKGEKKAFYBEEISSM 124
PONTVEDAKRLIGRKFNDPVVGSDMKLMPFQVINDAGKPKVIVSYKGEKKAFYBEEISSM 124
                                                                                                                         ESYAFNMKSAVGDEGLKDKISESDKKKILDKCSEVLSWLEANQLAEKEEFDHKRKELENM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGMAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMN
                                                                                                                                                                       ESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQV
                                                                                                                                                                                                                                                              NGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNAL
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302

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A; Title: Comparative analysis of the three major histocompatibility complex-linked A; Reference number: 154542; MUID:95012453; PMID:7927536
A; Accession: 165987
                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Rattus norvegicus (Norway rat)
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
;Accession: $41415; 168987
             3 KAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALN 62
                                                                                                                                                                                                                                                                EMBL:X77209; NID:g1814002; PIDN:CAA54424.1;
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                                                                     Mismatches
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A;Gene: hsc/3; hsc/0
A;Introns: 137/3; 188/3; 374/1; 441/3; 508/1; 585/3
C;Function:
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein C;Superfamily: heat shock protein 70
C;Superfamily: heat shock protein 70
C;Roywords: Aftp; molecular Chaperone
E;2-646/Product: dnaK-type molecular Chaperone hsc/3 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Wang, C.; Lee, M.R.
Blochem, J. 294, 69-77, 1993
A.Pitle: High-level expression of soluble rat hsc70 in Escherichia coll: purification
A.Peference number: 35506; MUID:93371384; PMID:8363588
A.Rocession: 33506
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R:0'Mblley K.; Mauron, A.; Barchas, J.D.; Redes, L.
Mol. Cell. Biol. 5, 3476-3483, 1985
A;Tille: Constitutively expressed rat mRNA encoding a 70-kilodalton heat-shock-like A;Reference number: IS7594; WID:68310877; PMID:3339319
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A; Residues: 2-40 <WAN>
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A; Residues: 1-646 <RES>
A; Cross-references: GB:M11942;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Sorger, P.K.; Pelham, H.R.B.
EMBO J. 6, 993-998, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Date: 29-Jan-1993 #sequence_revision C; Accession: S07197; 157594; S35606
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A; Residues: 1-646 <SOR>
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                                                                                                                                                   LNPQNTVFDAKKLIGKKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS 120
KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI 420
                  KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALLKRNSTI 420
                                                                           RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN 360
                                                                                                                                                                                                                                 IAYGLDKKVGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNH
                                                                                                                                                                                                                                                 IAYGLDRTGKGERAVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH 240
                                                                                                                                                                                                                                                                                                             SMYLTKMKETAEAYLGKTVTNAVVTVPAYFNDSQRQATKDAGTTAGLNVLRTINEPTAAA
                                                                                                                                                                                                                                                                                                                                       SMYLTKMKEIAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA 180
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85.8%;
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C/Function:
A;Description: in
C;Superfamily: he
C;Keywords: ATP;
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A; Molecula type: mRNA
A; Residues: 1-646 < SODD
A; Residues: 1-646 < SODD
A; Cross: references: (8107129; NID: 9861212;
A; Cross: references: (9107129; NID: 9861212;
This protein plays a role during
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C; Genetics:
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A; Accession: JC4853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Soulier, S.; Vilotte,
Gene 172, 285-289, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: heat shock protein 73
C:Species: Mus musculus (house mouse)
C:Date: 15-Aug-1996 *sequence_revision 18-Oct-1996 *text_change
C:Accession: JC4853
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Pred. No. 3.6
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C; Genetics:
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C, Punction: involved in protein fo
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                                                         KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI
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                                                                                                                                                                                                                                                                                SMVLTKMKEIAEAYLGKTVTNAVVTVPAYFNDSQRQAAKDAGTIAGLNVLRIINEPTAAA
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                                                                                    KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                               RFEELNADLFRGTLDPVEKALRDAKLDKSQIHDIVLVGGSTRIPKIQKLLQDFFNGKELN
                                                                                                                                        RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                                                                                                                                           IAYGLDKKVRAERNVLIFDLGGGTFDVSILTTEDGIFEVKSTAGDTHLGGEDFDNRMVNH
                                                                                                                                                                                                                                                                                                           SMYLTKMKEIAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA
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-	Oy 61 LMPONTYPDAKRLIGRKFGDPVYOSDMKHMPFQVINDGDKFKVOVSTKGETKAFYPEEIS 120 Db 61 MMPTNTYPDAKRLIGRREDAWYOSDMKHMPFQVINDGRFKVOVETKGETKAFYPEEVS 120
	QY 1 MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60 1: 1:
	Ouery Match 97.5%; Score 2856.5; DB 2; Length 646; Best Local Similarity 85.6%, Pred No. 53e-15); Length 646; Matches 553; Conservative 47; Mismatches 41; Indels 5; Gaps 3;
<u>⊢</u>	C;Function: involved in protein folding and assembling/disassembling of protein compl C;Superfamily: heat shock protein 70 C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
	A; Reference number: \$1280; MUD:91067440; PMID:251119 A; Reference number: \$1280; MUD:91067440; PMID:251119 A; Accession: \$1280 A; Accession: \$1280 A; Molecule type: DAA A; Residues: \$33-383:488-452:580-587 (LID)
	4402; NID:9300/3; FIDN:CAA38268.1; FID:9550/4
	KIMAXMELL, E.S. SUBSTANTIAN AUGUST 1990 A:Reference number: S50895
	A; Molecula type: protein A; Molecula type: protein A; Residues: 89-102;160-187;272-282;575-583;610-638 <ima></ima>
2	A/Title: Antibodies against 70-kD heat shock cognate protein inhibit mediated nuclear in Reference number: A44262; MUID:93007667; PMID:1332978
_к	A;Note: the authors translated the codon GAT for residue 97 as Asn R;Imanoto, N.; Matsuoka, Y.; Kurihara, T.; Kohno, K.; Miyagi, M.; Sakiyama, F.; Okada, Y J. Cell Biol. 19. 1047-1061 1992
	A.Molecule (Personal) A.Molecule (Peps: mRM) A.Rosidues: 1-646 <gis> A.Rosidues: 1-646 <gis> A.COSS-references: GB.M.9141; NID:q194034; PIDN:AAA37869.1: PTD:q309319</gis></gis>
	A, A.E.E.: Peresuphenical regulacion of a constitutively expressed mouse mana encoding a /A A;Reference number: A45935; NUID:880558/2; PNID:3334/18 A;Recession: A45935 A:Strains order integral
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	C;Species: Mus musculus (nouse mouse) C;Date: 30-Sep-1993 #sequence_revision 26-May-1994 #text_change 20-Aug-1999 C;Accession: A45935; A44262; S50895; S12831; S12831; S12832
	A43933 dnäK-type molecular chaperone hac70 - mouse N:Alternate names: heat shock cognate protein hsc70
	RESULT 15
	Db 601 KVCNPIITKLYQSAGGMPGGFPGGGAPPSGGASSGPTIEEVD 646
	QY 601 QYCNPIISGLYQGAGG-PGPGGFGAQGPKGGSGSGPTIEEVD 641
	OY 541 ALESYAPNKSAVEDBELIGKI.SEADKKVILDKCOEVISHLDANTLAEKDEPEHKRKELE 600 DD 541 SLESYAPNKATVEDEKI.GGKI.NOEDKOKI.LDKCNEII.SHLDKNOTAKKEEPEHOKELE 600 541 SLESYAPNKATVEDEKI.GGKI.NOEDKOKI.LDKCNEII.SHLDKNOTAKKEEPEHOKELE 600
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361 KSINPDEANNGANQAALIMODKSERVODLLLDVAPLSIGLEPAGGVMTVLIKRNTI 420
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                    601 QVCNPIISGLYQGAGG-PG--PGGF--GAQGPKGGSGSGPTIEEVD 641
                                                         541 SLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIISWLDKNQTAEKEEFEHQQKELE
                                                                          541 ALESYAFIMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE 600
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Copyright (c) 1993 - 2002 Compugen Ltd.
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(7) X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.	RP	sus scrofa sus scrofa
<pre>prepared from heat-shocked and non-heat-shocked human cells."; Nucleic Acids Res. 14:8933-8949(1986).</pre>	RI	nydra magnı pleurodeles
scription of a human hsp 70 heat shock gene by	RT	homo sapien
MEDLINE-87066768; PubMed-3786141;	2 R R	paracentrot
[6]	RN	drosophila
heat shock protein HSP/U."; Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).	RE	bos taurus
'Human major histocompatibility complex contains genes for the	RI	xenopus lae
Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;	R A	mus musculu
SEQUENCE OF 1-36 AND 360-424 FROM N.A.	RP.	cricetulus
[5]	RN	oncorhynchu
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."; Submitted (SED-1999) to the EMRI/GenBank/DDRI databases	RI RI	homo sapien
	RA	rattus norv
[4] SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).	RP KN	homo sapien
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.	RL	rattus norv
region.";	RT	mus musculu
nan maior high compatibility complex class	RA PM	mus musculu
Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,	RA	mus musculu
(hseala and hseals). Oin S., Shaffer T., James R., Ratcliffe	RA RA	rattus norv
(3)	RN	sus scrofa
Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).	RL	
"Conserved reatures of eukaryotic hsp/o genes revealed by comparison with the nucleotide sequence of human hsp70.":		bos taurus
	RA	
MEDLINE=86016721; PubMed=3931075;	R &	ption
[2]	RN	
Immunogenetics 32:242-251(1990).	~ 5	
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SEQUENCE FROM N.A. MEDLINE-9105806; PubMed-1700760;	R R P	ave a og printed,
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Mammalla; Eucherla; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	0 C	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	88	
Homo sabjens (Human)	000	
Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).	DE	
15-JUN-2002 (Rel. 41, Last annotation update)	DŢ.	
01-FEB-1994 (Rel. 28, Last sequence update)	DI G	
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by non-profit institutions as long as its content is in no way
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INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK
                           LNPQNTVFDAKKLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
                                                                                                MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDOGNRTTPSYVAFTDTERLIGDAAKNQVA
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TISSUE=Skeletal muscle;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
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   TUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HEPTOS STRAILIZE
PREEXISTENT PROPERIES AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHI
ORGANELLES. THE HEPTOS IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE P
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NOV-1997 (Rel.
JUL-1999 (Rel.
t shock 70 kDa)
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35, Last sequence up
38, Last annotation
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RESULT 3
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DT 01-NOV
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Best Local
HS72_BOVIN STANDARD;
Q27965; Q28122;
Q1-NOV-1997 (Rel. 35, Created)
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PROSITE: B01036: HSP70_3: 1.
ATP-binding: Chaperone: Heat shock; Multigene family.
SEQUENCE 641 AA: 70250 MM; 6D548263E98780F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; Hsp70; 1.
PROSITE; PS00297; HSP70_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
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                                                                                                                       LKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVCNPIIS
                                                                                                                                        LKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVCNPIIS
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Pred. No. 0;
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Query Match Best Local S Matches 47(

Similarity

57.78; 0,

Score 370; DB Pred. No. 0; 0; Mismatches

DB ļ.

Length 641;

0;

Gaps

0

Conservative

138

PVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLI 197

PVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLI

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                                                                                                                                                                       EMBL; U02892; AAA03451.1; -. EMBL; M98823; AAA30568.1; -. HSSP; P08107; 1HJO.
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Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
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Bovidae; Bovinae; Bo
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                                                                                                                                                         InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                        FÜNCTION. IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREXISTENT PROTEINS AGAINGT AGGREGATION AND MEDIARE THE FOLDING OF NEMLY TRANSLATED POLYREPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL FOLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY HARE INVOLVED IN SIGNAL TRANSUCCTION PROTEIN TRANSLOCATION WITH HSP90. THEY PARTICLATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE MONNATIVE COMPANYS IN COOPERATION WITH HSP90. THEY BOD EXTENDED PEPTIDE SECHENTS WITH A BET HYDROPHOBIC CHARACTER EXPOSED BY POLYPETIDES SECHENTS WITH A BET HYDROPHOBIC CHARACTER EXPOSED BY POLYPETIDES OFFICE TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STREES—THOUGED DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                            INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                        requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35, Last sequence update)
39, Last annotation update)
protein 2 (HSP70-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                           restrictions
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                        Pfam: PF00012: HSP70. 1
PRINTS: PR00301: HEATSHOCK70.
PRODOM: PD000089: HSP70. 1
PR0SITE: PS00239: HSP70. 1
PR0SITE: PS00329: HSP70. 3: 1
PR0SITE: PS00329: HSP70. 3: 1
                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMHD outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in oway modified and this statement is not removed. Usage by and for on movercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P34930;
                                                                                                                                                                                                                                                                                                                                                                INMUNOJENELICE 35:286-289(1992)

INMUNOJENELICE 3C:286-289(1992)

PREMITION IN CODERRATION MITH OTHER CHAPERORES, REPTOS STABILIZE PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLLING OF MEHLY TRANSLATED DOLYPEPITIDSS IN THE CYTOSOL AS MELL AS MITHIN ORGANIZLES: THESE CHAPERORES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECORDER NONATUVE COMPONATIONS OF CHARACTER STANSLATION OF CHEMPETIDE SCREENIS WITH A NET MYDOPHOBIC CHARACTER EXPOSED BY POLYPETIDES DURING TRANSLATION AND MEMBRARE TRANSLACION OR FOLLOWING STRESS INDUCED DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Heat shock 70 kDa protein 1 (HSP70.1).
ATP-binding; Chaperone; Heat shock; Multigene family. SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                                                                                           HSSP; P08107; 1HJO.
InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bouquet Y.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92175874; PubMed=1339404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peelman L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of a porcine HSP70 gene.";
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                                                                                                                                                                                 S35718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNALESYAFNMKSAVEDEG
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                                                                                                                                                                                                  M69100;
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S35718.
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Query Match
Best Local S
Matches 309
15-DBC-1998 (Rel. 37, Created)
15-DBC-1998 (Rel. 37, Last sequence update)
15-DBC-1998 (Rel. 37, Last annotation update)
Heat shock 70 kDa protein 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLIFDL 200
                                                                                     CERAE
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                                                                                                                                                                                                                                     MGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLI
                                                                                                                                                                                                                                                                        MGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLI
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                                                                                                                                                                                                                                                                                                                      LRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAIL 380
                                                                                                                                                                                                                                                                                                                                                                         RRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKA
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                                                                                     STANDARD;
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No. 1.
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CERAE Q28222; 15-DEC-1998 HS71

Cercopithecus aethiops (Green monkey) (Grivet). Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Cercopithecidae; NCBI_TaxID=9534; Cercopithecinae; Cercopithecus

SEQUENCE FROM N.A.

TISSUE-Kidney

MEDLINE-95080396; PubMed-7988690; Sainis I., Angelidis C., Pagoulatos G., Lazai Sainis II., Angelidis C., Pagoulatos G., Lazai "The has/0 gene which is slightly induced by inducible member of the hsp70 gene family."; Lazaridis heat ŝ the main virus

PERS LETE 135:283-286(1944)

THEN THE PROPERTION WITH OWNER CHAPBENNES, HSP70S STABILIZE PRENKTION. IN COOPERATION WITH COWNER CHAPBENNES, HSP70S STABILIZE PRENKTISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF MEMILY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITCHONOMORIA AND THE EMPORLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THERE ABLITY TO RECOGNIZE NUMBER IN ALL THESE PROCESSES THROUGH THERE ABLITY TO RECOGNIZE NUMBER UNDERTONE SECRETS WITH A NET HYDROPHOET CHARATERE EXPOSED BY POLYPEPTIDES DURING TRANSLATION, AND MEMBRANE TRANSLOCATION, OR POLLOWING

STRESS-INDUCED DAMAGE.

 -:- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY INDUCTION: BY HEAT SHOCK.

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RESULT
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Best Loc
Matches
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PRODOM: PR000089; HEB70.1.
PR0SITE: PS000297; HEP70.2: 1.
PR0SITE: PS000299; HEP70.2: 1.
PR0SITE: PS01036; HEP70.2: 1.
AIT-LINGING; Chaperone; Heat sh
SEQUENCE G.SB AA; 69220 MA;
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Q07439; P42853;
Q1-FEB-1995 (Rel
Q1-FEB-1995 (Rel
HIGHTO YEARS.

11 FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST BRIDGES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZATE. THE FOLDING OF NEWLY TRANSLAYED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZATES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
                                                                             STRAIN-Sprague-Dawley: TISSUE-Liver;
MEDLING-94368374; PubMed-8086479;
MEDLING-9436874; PubMed-8086479;
Lisowska K., Krawczyk Z., Widdak W., Wolniczek P., W
                                                                                                                                                MEDLINE-95012453; PubMed-7927536; Walter L., Rauh F., Guenther E.; Walter L. analysis of the three major histocompatibility linked heat shock protein 70 (Hs70) genes of the rat."; Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                   Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen Massa S.M., Sharp F.R.; "CDNA cloning and expression of stress-inducible rat and injured rat brain.";
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                   01.FEB-1995 (Rel. 31, Created)
01.FEB-1995 (Rel. 31, Last sequence update)
16.00T-2001 (Rel. 40, Last annotation updat
Heat shock 70 kba protein 1/2 (HSF70.1/2).
HSF70-1 AND HSF70-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; Hsp70. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                    STRAIN-LEW.1W/GUN;
                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                    MEDLINE-94096443; PubMed-8271311;
                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLL
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                                                                  gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X70684; CAA50019.1;
P08107; 1HJO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 175; DB
;; Pred. No. 4.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shock;
                                                                                                                                                                                                                                                                                                                                                                             Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D55076A0FFAB6AB3
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                                                                              Wisniewski J.;
t heat inducible
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Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                       HS71_MOUSE STAY
P17879; Q61689;
01-AUG-1990 (Rel. 1
01-NOV-1997 (Rel. 1
16-OCT-2001 (Rel. 4
Heat shock 70 kDa p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00
PROSITE; PS00
PROSITE; PS01
ATP-binding;
CONFLICT
                                                                                                                                                                                                               01-NUC-1990 (Rel. 15, Created)
01-NVC-1997 (Rel. 35, Last sequence upo
16-OCT-2001 (Rel. 40, Last annotation v
Heat shock 70 kpa protein 1 (HSP70.1)
HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
ProDom;
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     Perry M.D., Aujame L., Sht
"Structure and expression
Mus musculus.";
                                                                                          Gene
                                                                                                   expression
                                                                                                                              Hunt C., Calderwood
                                                                                                                                         MEDLINE-90236310;
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Ver-
Mammalla; Eutheria; Rodentia; Sciurognathi;
NCBI_TaxID=10090;
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                                          MEDLINE-94357449; PubMed-8076831;
                                                      TISSUE-Liver;
                                                                  SEQUENCE FROM
                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                     "Characterization and se
expression in mouse cell
                                                                                                                                                                                                                                                                                                                                                                   373
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                                                                                                                                                                                                                                                                                                                                                                                                                   313
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                                                                                                                                                                                                                                                                                                                                                                 AAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                   TLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYG
                                                                                          87:199-204(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                       N.A
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                           PubMed=2332169;
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100 17.8%;

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Score 114; DB 1; I Pred. No. 3.3e-107;

Length Indels

641;

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Mismatches

c

0;

Gaps

372 0

PRT;

641

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update)

update) (HSP70-1/HSP70-2).

Vertebrata; Euteleostomi;

Muridae;

Murinae;

Mus

sequence

lines

. ° cf

p

mouse

hsp70

gene

and

its

Shtang S., Moran L.A.; ion of an inducible HSP70-encoding

gene

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modified and this statement
entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                        L; L16764; AAA17441.1; -.
L; X77208; CAA54423.1; -.
L; X77207; CAA54423.1; -.
L; X77207; CAA54328.1; -.
L; X74271; CAA55328.1; -.
P; P08107; 1HJO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THROUGH THEIR ABILITY TO RECOGNIZE NOWARTUNE COMPORATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGENTS MITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                  PF00012; HSP70;
                                                                                                                                      3; PR00301; HEATSHOCK70.
18; PR0000089; HSp70; 1.
18; PS00297; HSP70_1; 1.
18; PS00329; HSP70_2; 1.
18; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 email to license@isb-sib.ch).
                                                                                        Chaperone; Heat
71 72
                         408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
70163 MW;
                     shock; Multigene family.
KR -> NG (IN REF. 3).
D -> H (IN REF. 2 AND 3)
G -> A (IN REF. 3).
D02D96751C868583 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions
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Gene

AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

a collaboration

OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION

e 146:273-278 (1994).

FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGRECATION AND MEDIATE THE FOLDING OF NEMLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS MITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE MONNATIVE CONFORMATIONS OF

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RESULTANT HERSOLT HER STAND HE STAND HER STAND
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Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              061696; 061697;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
Heat shock 70 kbm protein 3 (HSP70.3) (Frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
HS73_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom: PD000089; Hsp70; 1.
PROSITE: PS00297; HSP70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
PROSITE: PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstaion the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for convertial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                               Lowe D.G., Moran L.A.;
"Molecular cloning and analysis of DNA
"Molecular cloning and analysis of DNA
Mr = 68,000 heat shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                   HSP70-3 OR HSP70A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M35021; AAA37864.1; -.
EMBL; M76613; AAA57233.1; -.
EMBL; JH0095; JH0095.
Perry M.D., Aujame
                         MEDLINE-94357449;
                                                                                                                                                                                                              MEDLINE-86111900; PubMed-2868009;
                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P08107; 1HJO.
MGD; MGI:99517; Hsp70-1.
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                                                           SEQUENCE OF 155-420 FROM N.A.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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627
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                         PubMed-8076831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69994 MW;
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0; Mismatches
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P -> PP (IN REF. 1).
1; 41475360F6749F2F CRC64;
                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                    mRNAs.";
   Moran
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(Fragment).
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                                                                                                                                                                  three mouse
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Mus musculus.";
Gene 146:273-278(1994)
-i- FUNCTION: IN COOPE
                                                                                                      "Structure and
                                                                                                     expression
                                                                                                      of an
                                                                                                      inducible HSP70-encoding gene
                                                                                                      from
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- FUNCTIONS: IN COOPERATION WITH OTHER CHAPERONES, HEP70S STRALLIZE
 PREEXISTENT PROPERIN AGAIST AGGERATION AND MEDIATE THE FOLDING
 OR NEMLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS MITHIL
 ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
 THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE COMPORMATIONS OFF
 OTHER PROTEINS. THEY BIND EXTENDED PETIDES DEMENTED WITH A NET
 OTHER PROTEINS. THEY BIND EXTENDED BY POLYPEPTIDES UNLING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED S STABILIZE
 THE FOLDING
 LL AS WITHIN
- INDUCTION: BY HEAT SHOCK.
 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY

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PROSITE;
SEQUENCE
                                          ATP-binding; Chaperone; Heat shock; Multigene family
                                                             PROSITE;
                                                                                                         ProDom;
                                                                                                                      Pfam; PF00012; HSP70;
                                                                                                                                     MGD; MGI:96244; Hsp70-3.
InterPro; IPR001023; Hsp70.
                                                                                                                                                                               EMBL; M12571;
EMBL; M12572;
                                                                                                                                                                     P08109; 1CKR.
                                                         P500012; HSP70; 1.

P5000089; HSP70; 1.

; PS00297; HSP70_1; PARTIAL.

; PS00329; HSP70_2; PARTIAL.

; PS01036; HSP70_3; 1.
188
420 #
                                                                                                                                                                                 AAA57235.1;
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ĀĀ;
              188
46292 MW;
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                ý
5DA1C6155C7B16B5 CRC64;
                a
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δÃ Matches Query Match 333 Local .08 Similarity Conservative 12.5%; 0; Score 80; Pred. No. Score Mismatches DB 1; 7e-73; 0, Length Indels 420; 0; Gaps

0

393 LLDVAPLSLGLETAGGVMTA 412 DLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLL 392 DLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLL 171

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172

LLDVAPLSLGLETAGGVMTA 191

HS71

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RESULT
                                                                                                                                                                                                                            Oryzias latipes (Medaka fish) (Japanėse ricefish)
Ekaryota, Metazoa, Chordata; Craiata; Vertebrata; Buteleostomi;
Atliopierygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii, Percomorpha; Atherinomorpha;
meloniformes), Adrianichthyldde; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS71_OR
Q918F9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORYLA
Naruse K., Sakuragi M.;
"Medaka HSP70 gene cloning.";
"Medaka HSP70 gene cloning.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY; BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heat shock 70 kDa protein 1 (HSP70-1)
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID-8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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This SWISS-PROT entry is copyright. between the Swiss Institute of Bio

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Bioinformatics and

through

a collaboration ~

European Bioinformatics Institute.

There are no restrictions

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                                                                                                                                                                                                                                                                                                                                                                                           "Identification and sequence analysis of a new member of the mouse HSP70 gene family and characterization of the unique cellular and developmental pattern of expression in the male gern line.";

MOL. CEIL BLO. 8:292-2921(198).

MOL. CEIL SELO. 8:292-2921(198).

MOL CEIL SELO. 8:202-2921(198).

MOL SELO. 8:202-292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions us with a modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                             HSSP;
                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Nus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1917.15;
01-MUG-1990 (Rel. 15, Created)
01-MUG-1990 (Rel. 15, Last sequence update)
01-MUG-1990 (Rel. 35, Last sequence update)
01-MUG-1997 (Rel. 35, Last annotation update)
101-MUG-1997 (Rel. 35, Last annotation update)
Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2).
HSPA2 OR HSP70-2 OR HCP70.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom: PD000089: Hap70: 1.

PROSITE: P800329: HaP70_2: 1

PROSITE: P800329: HSP70_3: 1

PROSITE: P801036: HSP70_3: 1

ATP-binding: Heat shock; Multigone family:
                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zakeri Z.F., Wolgemuth D.J., Hunt C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=88302212; PubMed=3405224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS72_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P08109; 1CKR
                        MGD; MGI:96243; Hsp70-2
                                                                                                 EMBL; M20567; AAA37859.1;
                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 IGIDLGTTYSCVOFORGKELIANDGUNRTJESYVAFTDTERLIGDANKUVALNP
9 IGIDLGTTYSCVOFORGKELIANDGUNRTJESYVAFTDTERLIGDANKUVALNP
                                                                                                                                                                                                             European Bioinformatics Institute. There are no restrictions on by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                             OF MEIOSIS
                                                                            S10859;
                                                P19120; 1ATR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF286875; AAF91485.1;
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                                                                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics and the
IPR001023; Hsp70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   639
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                                                                         S10859.
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Pred. No.
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A CONTRACTOR REPORT OF THE PROPERTY OF THE PRO
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HS72_RAT
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Best Local S
Matches 55
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation and nucleotide sequence analysis of the rat testis-specific major heat shock protein (HSP70)-related gene."; Esstis-specific major heat shock protein (HSP70)-related gene."; Biochim. Blodyls. Acta 104:893-99(1990).

Biochim. Blodyls. Acta 104:893-99(1990).

ESSTATISTE PROTEIN AGAINST AGGREGATION AND HEDDING THE FOLDING OR HERIX TRANSLATED POLYMEPTIDES IN THE CYPOSOL AS EALL AS WITHIN ORGANIZILES. THESE CHAPENORES PARTICIPATE IN ACTIONATION OF OTHER FOOTEINS. THEY BLOD EXTRADED POPTIDE SECHENTS WITH A NET OTHER EXPOSED BY POLYMETTIDES DEADNING TRANSLATION ON THE HEAD OF THE SECOND POPTIDE SECHENTS WITH A NET OTHER EXPOSED BY POLYMETTIDES DURING TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS72_RAT
P14659;
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PROSITE: PS00207: HBPT0_1: 1.

PROSITE: PS00207: HBPT0_2: 1.

PROSITE: PS01035: HBPT0_2: 1.

PROSITE: PS01035: HBPT0_3: 1.

PROSITE: PS01035: HBPT0_3: 1.

PROSITE: PS01035: HBPT0_3: 1.

PROSITE: PS01033: AA; 6974-0 WM; E7F9040F2AB138D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the BMBL outstation. The Burgean Hoinformatics institute, There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-90122930; PubMed-1688714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-ARR-1990 (Rel. 14, Last sequence update)
Ol-OCT-1996 (Rel. 34, Last sequence update)
Heat shock-related 70 kpa protein 2 (Heat shock protein
                                                                                                                  BRANTS; PR00301; HBATGHOCK70.
PRODOM: PD000089; HB970; 1.
PROSITE; PS00297; HB970_1; 1.
PROSITE; PS00329; HB970_2; 1.
PR0SITE; PS00339; HB970_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific heat shock protein-related) (HST).
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                                                               SEQUENCE
                                                                                            Spermatogenesis
                                                                                                                                                                                                                                                                                                   InterPro; IPR001023; Hsp70. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                PIR; S08211; S08211.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; x15705; CAA33735.1; ~.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 61
                                                                                                                                                                                                                                                                                                                                                                       P19120; 3HSC
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Conservative 0;
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                                                               69528 MW;
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    Score 55;
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                                                               6878CA5C2EEBF7DA CRC64;
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. 2.4e-47;
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Matches
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PRODUCT: P0000089; HSp70; 1.
PROSITE: PS00299; HSP70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
PROSITE: PS00329; HSP70_3; 1.
ATP-binding; Heat shock; Multig
                                                                     HD72.HUMAN STANDARW,
HB72.HUMAN STANDARW,
HB72.HUMAN STANDARW,
HB72.HUMAN STANDARW,
D1-00T-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence up
01-FEB-1994 (Rel. 28, Last annotation
Heat shock 70 kba protein (HSP70).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SNISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86304452; PubMed-3017985; Morimoto R.I., Hunt C., Huang S.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
NCBI_TaxID=9606;
                 Mammalia; Eutheria;
                                Eukaryota; Metazoa;
                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A25646; A25646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J02579; AAA48825.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 261:12692-12699(1986).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Organization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P08106;
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                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                       6 AIGIDLGTTYSCYGYFQHGKYEIIANDQGNRTTPSYYAFTDTERLIGDAAKNQVA 60
                                                                                                                                                                                                                                                                      AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P08109; 1CKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene.".
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55; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                 634 AA;
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                   Primates;
                                Chordata;
                                                                                                                                                                                                                                                                                                                                                          8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                 69750 MW;
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0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family
                                                                                                                                                                                                                                                                                                                                         Score 55; DB
; Pred. No. 2.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                           0;
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; Mismatches
                 Catarrhini;
                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 4270F7F08D365AEB CRC64;
                                                                                      on update)
(Heat shock
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and transcription
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hes 0;
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                 Hominidae;
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iption of the
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HS73_RAT
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Best Local
                                                 HS73_RAT
P55063;
01-OCT-1996
01-OCT-1996
01-OCT-1996
                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
101-OCT-1996 (Rel. 34, Last annotation update)
Heat shock 70 kDa protein 3 (HSP70.3).
                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0301; HEATSHOCK70.
PROD000; PD0000089; HSP70; 1.
PROSITE; PS002297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01016; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
Rattus norvegicus (Rat)
                 HSP70-3.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Chaperone; Heat shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 140560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00012; HSP70;
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                          266
639 AA;
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                                                                                                                         STANDARD;
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70021 MW;
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                                                                                                                                                                                                                                                                                                         Score 55;
Pred. No.
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2.4e-47
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Length 639 Indels

0; 60

Gaps

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-95130116; PubMed-7829106;

A Bonnycastle L.L.C., Yu C.-E., Hunt C.R., Tra

Bonnycastle L.P.C., Yu C.-E., Hunt C.R., Tra

Bonnycastle L.P.C., Yu C.-E., Hunt C.R., Tra

Weber J.L., Patterson D., Schellenberg G.D.;

"Cloning, sequencing, and mapping of the hur

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"The shock process of the sequence of the seque
                                                                                                                             use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commentities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROUX A.F., MQUYEN V.T.T., SQUITE J.A., COX D.W.;

"A heat shock gene at 1402: mapping and expression.";

Hum. Mol. Genet. 3.1819-1822(1994)

HUM. MOL. GENET. 3.1819-1822(1994)

HUM. THE COMPRATION WITH OTHER CHAPENONES, HSP70S STABILIZE

I-PHRYICH PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING

OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES ARTICIPATE IN ALL THESE PROCESSES

THROUGH THEIR ABILITY TO RECORDE NOWANIVE CONFORMATIONS OF OTHER PROTEINS. THEY HIMD EXTREMED PETIDE SEGMENTS WITH A NET

HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLACTION OR FOLLOWING STRESS-INDUCED DAMAGE.

AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

1-1 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HS7H_HUMAN STANDARD: PR 934931, 0900M1; Ol.FEB-1994 (Rel. 28, Created) Ol.FEB-1994 (Rel. 28, Last seque 16-CGT-2001 (Rel. 40, Last and Heat shock 70 kDa protein 1-HOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0301; HEATSHOCK70.
PRODOM: PD000089; HSP70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00299; HSP70_2; 1.
PROSITE; PS001036; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and the EMBL outs, warprofit institutions as long as its content is in entities requires a license agreement. Usage hyperson or send an email to license agreement.
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linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:225-330(194).

                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-91055806; PubMed-1700760;
Milner C.M., Campbell R.D.;
*Structure and expression of the
                                                                                                                                                                                                                                                                                                                                                                           HOMO Sapiens (Human).

---- Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSPAlL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00012; HSP70;
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InterPro; IPR001023; Hsp70.
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                                       SEQUENCE FROM N.A.
                                                                                                             [mmunogenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIGIDLGTTYSCYGYFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
    Qin S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                             expression of the 32:242-251(1990).
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Madan A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28, Last sequence update)
40, Last annotation update)
protein 1-HOM (HSP70-HOM).
                                                                                                                                                                                                                                                                                                                                                            Primates;
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%; Pred. No. 2.4
0; Mismatches
    Dickhoff R.,
                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8C77AA9FD98B9252 CRC64;
                                                                                                                                           three MHC-linked HSP70 genes. ";
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    Madan A., Hicks P.,
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Best Local :
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS: PR00301; HEATSHOCK70.
Probom; PD000089; Hsp70; 1.
PROSITE: PS00297; Hsp70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
PROSITE: PS01336; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loretz C., Ratcliffe A., Abbasi N., Shaffer T., "Sequence of the human major histocompatibility region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:5234; HSPA1L.
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HSSP; P08107; 1HJO.
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"Polymorphic analysis of the three MHC-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Multigene family; Polymorphism.
VARIANT 493 493 T -> M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00012; HSP70;
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                                   AIGIDLGTTYSCYGYFQHGKYEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
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AIGIDLGTTYSCYGYFQHGKYEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
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/FTId=VAR_003820.
V -> A (IN REF. 2).
P -> T (IN REF. 2).
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2.4e-47;
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Search completed: December 4, 2002, 16:51:59
Job time: 15 secs



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score greater than or equal to the score of the result being pu
and is derived by analysis of the total score distribution.
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AAE12986
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AAB823252
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                   Human heat shock 7
Human heat shock p
Human Hsp70 family
Human heat shock p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemical markers of human endometrium – useful for, e.g diagnosis of hyperplasia and adenocarcinoma {\bf r}
                                                                                                         WPI; 1998-207057/18
                                                                                                                                                            Byrjalsen I,
                                                                                                                                                                                                                                                                              08-APR-1997;
06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                 05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09810291-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
2D gel electrophoresis; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW54349;
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AAU75102	AAB82535	AAE12987	AAB23651	AAB23649	AAY17408	AAY17407	AAW54364	AAR03927	ABG08625	ABG07786	ABG06754	AAG01506	AAR03930	AAR43002	AAR03928	AAB44074	AAB09885	AAY88413	AAY88412	AAB23650	AAR43004	AA009021	AAY88411	ABG38310	AAM04265	AAM29034	AAM16552	AAM68725	AAM56349	ABB20960	ABB35536	ABB30362	AAR03929	AAB09886
shock protei	shock	Human Hsp70 family	heat shock			Human heat shock c	Heat shock cognate	Rat HSP (rathsp70)	Novel human diagno	Novel human diagno	Novel human diagno	Human secreted pro	Gallus gallus HSP	Mouse SLIP1 homolo	Xenopus laevis HSP	Human cancer assoc	Hsp70 C-terminal 9		Human heat shock p	Rat heat shock pro	Mature mouse sperm		Human heat shock p	Human peptide enco	#2947	#3071	de #29		Human brain expres	Protein #2959 enco	#304		to.	Hsp70 C-terminal 2

ALIGNMENTS

Human heat shock 70 kD protein 1. 14-AUG-1998 (first entry) AAW54349 standard; protein; 641 AA

CLINICAL & BASIC Fey SJ, 97GB-0007132 96GB-0018600 97WO-GB02394 Larsen Ρ, RES

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immune response; infectious
                               ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte;
                                                                             Human
                                                                                                                     05-JAN-2001
                                                                                                                                                                                                  AAB23652 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                 QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTKQTQIFTTYSDNQPGVLTQVYEGERAMTKDNNLLGREELSGIPPAPRGVPQIEVTFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDG1FEVKATAGDTHLGGEDFDNRLVNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMVLTKMKETAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA
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                                                                          heat shock protein Hsp70.1 protein sequence SEQ
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Sequence

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disease; malaria; cytotoxic T cell,

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cytostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
                                 Shinbara N,
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                                                                                                      19-FEB-1999;
                                                                                                                                       18-FEB-2000;
                                                                                                                                                                         24 - AUG - 2000
                                                                                                                                                                                                          WO200049041-A1
2000-543748/49
                                                                  SUMITOMO ELECTRIC IND
                                 Udono H,
                                                                                                                                       2000WO-JP00941
                                                                                                      99JP-0041535
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The present invention describes a fused protein (T) prepared from a peptide containing a CTL (cytotoxic T lymphoxyte) epitope recognised by cytotoxic T cells and a protein containing the Affress dominate shock protein. Also described are: (1) a drug composition containing (T) as artire ingredient; (2) a DNA encoding (T); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the protein vector of (3); (1) has cytostatic, immunostimilant and protein containing the DNA of (2); and (4) a transformant which can retain the protein sector of (3); (1) has cytostatic, immunostimilant and protein compositions in preventing and/or treating interctions diseases such as majaria or cancer e.g. to provide systemic immunity against leakaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention. Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer Claim Page 46-48; 72pp; Japanese

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Matches 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
361
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KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                  KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI 420
                                                                                   RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                                                                       FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
                                                                                                                                                                                                         IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
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                                                                                                                                                                                                                                                                                                                                                                                                                MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
                                                                  REELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                                                       FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
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RESULT 3
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peptide binding fragments of heat shock proteins (HSB9) and non-
covalent complexes of HSB9 peptide-binding fragments (HBBF) in non-
covalent association with antigenic molecules. Vaccines comprising
peptide fragments of the invention may be used to stimute an
immune response, in particular cytotoxic cell responses against
cells infected with viruses (including hepatitis type A. B and C.,
influenza, varicella, adenovirus, herpes simplex (HSV) type I and
type II, rinderpest rhinovirus, echovirus, rotavirus, respiratory
                                                                                                                                                                                              Vaccine compositions for vaccinating against cancers and infections comprises peptide-binding fragments (PBES) of heat shock proteins (HSPS) and non-covalent complexes of PBES of HSPs and antigenic
                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat shock protein; HSP: HSP peptide-binding fragment; HPBF; vaccine; cytotoxic T cell response; hepatitis virus; herpes simplex virus; human immunodeficiency virus; barteria; Mycobatceria; Rickettsla; protozoa; Laishmani; Trypanosoma; intracellular parasite; Chlamydia;
                                                                                                                                                       Disclosure; Fig 1C;
                                                                                                                                                                                    molecules
                                                                                                                                                                                                                                                                                                                                                  20-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sarcoma; carcinoma; cancer; human; Hsp70 homologue; Hsp71.
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                                                                                                                      invention relates to pharmaceutical compositions comprising
                                                                                                                                                                                                                                                             2001-656559/75
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                                                                                                                                                                                                                                                                                                                       SRIVASTAVA P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family homologue,
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402..4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
391..615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..442
                                                                                                                                                     39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Peptide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Central core of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "P-helix motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain.
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Query Match
                                                                                                                                                                                                                                                                                                                meeasles virus, rubella virus, polio virus, HIV-1, and HIV-III, bacteria including (Including Mycobacteria, Rickettsia, Mycoplasma, Meisseria and Legionella), protozoa (including Islabmani, Kokzidioa and Trypanosoma) and intracellular parasites (including Chlamydia and Rickettsia). The vacches may be used to treat cancers such as human
                                                                                                                                          papillary carcinoma, papillary adenocarcinomas, medullary carcinoma, cystadenocarcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma and embryonal
                                                                                                                                                                                                                         sarcomas and carcinomas, panoreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma delenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma,
                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               syncytial virus, mumps virus, papova virus, papilloma virus, arbovirus, cytomegalovirus, echinovirus, huntavirus, coxsackie
                                                                                                                      carcinoma.
                                                                                                              The present sequence is human Hsp70 family homologue,
                                                               641 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus.
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Local
           MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
                                           641;
                                                     Similarity
                                         100.0%;
ilarity 100.0%;
Conservative
                                           0;
                                                     Score 641;
Pred. No. 0;
                                           Mismatches
                                                               DB
                                                               22;
                                           0;
                                                              Length
                                           Indels
                                                               641;
                                           0,
                                         Gaps
 60
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Matches

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241 181 181 121 121 61 61 FVEEFKRKHKKDISQNKRAVRLRTACERAKTILSSSTQASLEIDSLFEGIDFYTSITRA LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH SMYLTKMKEIAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS ${\tt IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH}$ SMYLTKMKETAEAYLGYPYTNAYITVPAYFNDSQRQATKDAGYTAGLNYLRITNEPTANA 300 240 240 180 180

421 PTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDI 480

DANGILNYTATDKSTGKANKITITNDKGRLSKEEIERMYQEAEKYKAEDEYQRERVSAKN

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무 õ 541 541 ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLABKDEFEHKRKELE ALESYAFINKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE 600

601 QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD

643

QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD 641

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RESULT 4 AAB82534 ID AAB

AAB82534 standard; Protein; 641 Ą

PXXXX AAB82534;

17-SEP-2001 (first entry)

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Matches 641
                                                                                                                                                                                                                                                                             The present sequence is that of human heat shock protein (HSP) HSP1, an inducible form of a HSP10 family protein. The invention relates to complexes of peptide-binding fragments of HSPs with antiqueic molecules and their use in immunotherapy for the treatment of infectious diseases and cancer. Claimed methods of treating or preventing cancer/infectious diseases involve culturing a cancer cell/infected cell transformed with a nucleic acid encoding a HSP peptide-binding domain, recovering complexes of the HSP fragments noncovalently associated with peptides from the cancer cell/infected complexes. These methods can cell, and administering the recovered complexes. These methods can
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition, used to treat or prevent infection or gracer, comprises a complex comprising a heat shock protein-binding fragment associated with a molecule displaying antigenicity of an
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 46; Fig 1C; 106pp; English.
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-457506/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2001; 2001WO-US01781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200152791-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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            181
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                                                                                                                                                                                                                                                                                                                                                                                                                            infectious agent or cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; vaccine.
                                                                                              61
                                                                                                                  61
                                                                                                                                                                                               Local Similarity
                                                                                                                                                  1 MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
                                                                                                                                                                                                                                            Hsp71 perfusive any the recovered complexes. These methods can 400-440 of the present sequence, i.e. the peptide-binding fragments comprising amino acids 391-615 400-440 of the present sequence, i.e. the peptide-binding ain and peptide-binding core.
                                                                                           IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
                        IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
                                                    SMVLTKMKE IAFAY LGYPVTNAV ITVPAY FNDSQRQATKDAGVI AGLNVLRI I NEPTAAA
                                                                         SMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA 180
                                                                                                                                       MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heat shock protein
                                                                                                                                                                                                                             641 AA;
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ilarity 100.0%;
Conservative
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/note= "beta-helix motif"
400..440
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391..615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "peptide-binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "peptide-binding core"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hsp71
                                                                                                                                                                                    0;
                                                                                                                                                                                             Score 641;
Pred. No. 0;
                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                        DВ
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AAB23252
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                                                             Examples; Fig 16B;
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Human Hsp72 (heat shock protein
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Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
                                                                                                                                                                                                                                                                                                               QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
                                                                                                                                                                                                                                                                                                                                                         QVCNPIISGLYQGAGGPGGPGGFGAQGPKGGSGSGPTIEEVD
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expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.

17-MAR-2000; 2000WO-US07350

9905-0125046

(PHYL-) PHYLOGENY INC

Sherman

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WPI; 2000-647056/62

Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,

77pp; English

The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses HBP72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of HBP72 contacted with the test compound under optimum

05-JAN-2001

(first entry)

heat

shock protein Hsp70

protein sequence

SEQ

ij NO:5. AAB23653 standard; protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC conditions to allow the two components to interact and bind, forming a CC complex which is detected the invention also relates to a method of CC identifying compounds that inhibit Happ?-moddated JMR phosphatas of CC activation, comprising contacting a test compound with no sillability of the CC determining if the compound inhibits JMR, phosphatase activity of the CC invention additionally encompasses compositions comprising an inhibitor CC of Happ? or JMR phosphatase activity are used in the compound inhibits JMR, phosphatase activity are used in the compound of the compounds inhibitor CC inhibitions of Happ? or JMR phosphatase activity are used in the compounds of the compounds dentified as CC inhibitions of Happ? or JMR phosphatase activity are used disorder such as cancers (e.g., pickagenia, jymphoma, solid tumours such as acromas and CC carcinomas, breast cancer, prostate cancer, prostate cancer, but the compounds that inhibit Happ? cfunction are administered to treat promitions that the compounds that inhibit Happ? cfunction are administered to a patient conficultion of activity relative to normal levels The present sequence represents we haven in the exemplifications of the invention.
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Matches 624;
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QVCNPIISGLYQGAGGPGPGGFGA
                                 QVCNPIISGLYQGAGGPGPGGFGA
                                                                                   ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
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                                                                ALESYAFNMKSAVEDEGIKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
                                                                                                                                  DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN
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RESULT 6 AAB23653

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Matches 632;
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a fused protein (1) prepared from a peptide containing a CUL (cytotock T lymphocyte) epitope recognised by peptide containing a the cytotock T lymphocyte) epitope recognised by cytotock T cells and a protein containing the Aprase domain of a heat shock protein. Also described are: (1) a drug composition containing the as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the protein plant of (2); (1) has cytostatic, immunositiniant and protein rective and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for during some compositions in preventing and/or treating infortious diseases such as malaria or cancer e.g. to provide systemic immunity against seukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fused protein capable of inducing cellular immune response, useful active ingredient for drug compositions in preventing and/or treat infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AffPase: Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
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KHKKDISQNKRAVRRERTACERAKRTESSTQASLEIDSLFEGIDFYTSITRARFEELCS
                                                                                                                     KETAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDR
                                                                                                                                                                                 FDAKRLIGRKFGDPVQQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKM
                                  TGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKR
                                                                  TGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKR
                                                                                                  KEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDR
                                                                                                                                                                   FDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKM
                                                                                                                                                                                                                                   GIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTV
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                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 49-52;
                                                                                                                                                                                                                                                                                                                                                                      640 AA;
                                                                                                                                                                                                                                                                                                    Conservative
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99.7%;
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- ANY SERVICE OF THE PROPERTY 
                                                                             This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21,3-6 and 14922-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of Stress and response and diagnosis of stress diseases including the stress and response and diagnosis of stress diseases including
                                                                                                                                                                                                                                                                                                                                                                                  Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; heat shock protein; HSP70; chromosome 5p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY88409 standard;
    Sequence
                                                             rheumatisms, schizophrenia,
                                                                                                                                                                                                                                                                                                Examples; Fig 2; llpp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOKE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       depression; nephrotic syndrome; SHSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human heat shock protein SHSP70 amino
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)B; AAA15621.
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                                                    depression and nephrotic syndrome
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Matches 553; Conserv
            N-PSDB; AAA15622
                     WPI; 2000-264458/23
                                           (HOKE-) HOKEN KAGAKU KENKYUSHO
                                                                   01-JUN-1995;
                                                                                         01-JUN-1995;
                                                                                                                07-MAR-2000
                                                                                                                                     JP2000069999-A
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                depression;
                                                                                                                                                                                           Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia;
                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                                                                                                                                                                                PKGGSGSGPTIEEVD
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                                                                                                                                                                                                                            heat shock protein
                                                                                                                                                                                nephrotic syndrome;
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                                                                   95JP-0158581
                                                                                         99JP-0257146
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Best Local S
Matches 553
Human; heat shock protein 70; HSP70; primer; probe; intracellular; abnormal transcription; acute; chron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6921.3-2: and 14922-24. The invention relates to the abnormal transcription of introcellular HSP70mRM under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumantisms, schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abnormal transcription of intracellular {\tt HSP70mRNA} under acute and chronic continuous load of stress in a human being and its application
                                                    Human heat shock protein 70
                                                                                 24-OCT-1997
                                                                                                                                                 AAW10065 standard; Protein; 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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MKHPPQVINOGDKPKVQVSYKGETKAFYPEEISSMVLTKNKEIABAYLGYPVTNAVITV 60
                                                                                                                                                                                                                                                                                                KKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVCNPIISGLYGGAGGPGPGGFGAQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTA
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                                                                                                                                                                                                                                                                PKGGSGSGPTIEEVD 641
                                                                                                                                                                                                                                                                                                                                KKKYLDKCQEVISWLDANTLAEKDEFEHKRKELEQVCNPIISGLYQGAGGPGPGGFGAQG
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Pred. No. 2.3e-313;
0; Mismatches 1;
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  chronic; sustain
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    sustained;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The cDNA encoding the present sequence, human heat shock protein (HSP70), is located on human chromosome by 21.3-22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the Ahnormal transcription of intracellular HSP70 mRNA in human acute and chronics ustained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of abnormal transcription specific primer or probe, used in dechronic sustained stress load
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N-PSDB; AAT58086.
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                  Homo sapiens
                                               depression; nephrotic
                                                               chromosome 14q22-24; transcription; rheumatism; schizophrenia
                                                                                                               Human heat shock protein HSP70
                                                                                                                                                 31-JUL-2000
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                                                                               Human; heat shock protein; HSP70; chromosome 6p21 3-22; stress;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTV
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Pred. No. 1.7e-277;
                                                                                                               amino acid sequence
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Best Local S
Matches 361
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Heat shock protein 70; Hsp70; NF-kappaB; transplant rejection;
                                                            AAB09886;
                                                                              AAB09886 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                  Hsp70 C-terminal 244 amino acid polypeptide sequence
                                        06-NOV-2000
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                                                                                                                                                                                                                                                                                                                 KEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDR 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 AA;
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                                       (first entry)
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99.7%;
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Pred. No. 1.3e-243;
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Best Local
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30-AUG-1990
                   AAR03929;
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                                                                                        241
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                                                                                        EEVD 244
                                                                                                            EEVD 641
                                                                                                                                                                       MVQEAEKYKAEDEVQRERVSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEV
                                                                                                                                                                                                                244 AA;
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Claim 6; Page 17; 37pp; English.
                                                              heat shock protein, useful in tautoimmune diseases and cancer
                                                                                         Intracellular targeted delivery of compounds using the 70 kiloDalton heat shock protein, useful in the treatment of transplant rejection,
                                                                                                                                                                                                                                                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                          98US-0109872
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US27244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory disease; cancer; vascular disease.
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The present sequence is the C-terminal 244 amino acids of the 70kD heat shock protein (Hsp70). This sequence was used in a fusion protein with the p50 subunit of transcription factor MR-Kappan, the sequence of which is indicated in the specification as being SEQ ID No: 1, but which is not given. This fusion protein was created in order to determine the cability of the Hsp70 sequence to direct other proteins into the cell. It was shown that Hsp70 fragments are able to direct other proteins into the cell, a feature which can be used in the treatment of transplant crejection, autoimmune diseases such as rheumatoid arthritis, multiple csclerosis, diabetes, asthma, inflammatory breads portasis, carves' disease and vitelyo, inflammatory disease, poortasis, or stepartials, pancrestitis and adult respiratory disease, syndrome, cancer, vascular diseases (wich as restemosis and atherosclerosis) and DNA and RNA viral replication diseases (including herpes).

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38.1%;
Score
Pred.
. 244;
DB 21;
1.6e-227
     Length 244
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hes	hes 244; Conservative 0; Mismatches 0; Indels 0; Gaps		0;
398	398 PLSLGLETAGGYMTALIKRNSTIPTKQTQIFTTYSDNQPGYLIQVYEGERAMTKDNNLLG 457	57	
-	PLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLG 60	J	
158	458 RFELSGIPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIER 517	7	

120

ISMLDANTLAEKDEFEHKRKELEQVCNPIISGLYQGAGGPGAGGFGAQGPKGGSGSGPTI
SMLDANTLAEKDEFEHKRKELEQVCNPIISGLYQGAGGPGFGGFGAQGPKGGSGSGPTI

240 637

AAR03929 standard; Protein; 640

(first entry)

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      own amino acid residues,
including "O" (?) at now
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                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                 Mycobacteria
                                                                                                                                                                                                                                                                                                           vaccines and
                                                                                                                                                                                                                                                                                                                      The proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2.1-2.14; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dragon E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CODO-) CODON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hsp70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
              328
                                                                                                                                 148
                                                                                                                                                      148
                                       268
                                                                                   208
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                                                                                                                                                                              88
                                                                                                                                                                                             88 KHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                      organisms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oteins homologous to heat shock proteins from Trypanosoma cruzi - use vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 uding "0" (7) at position 640.

2 provides an alignment of heat shock proteins from a variety

4 provides an alignment of Mayasp70 - AAR03922);
                                                                                 SILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTAC
                                                                                                                               1990-115820/15
KAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMGDKSEN
                                                                                                      SILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                   ERAKRTLSSSTGASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLD
                                                         ERAKRTLSSSTOASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLD
                                                                                                                                                                             KHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVP
                                                                                                                                                                                                                            525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heat shock
                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                        640 AA;
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                       6. Rat rattus (rathsp?0 - AAR03927);
7. Xenopus laevis (x170 - AAR03928);
8. Homo sapiens (humhsp?0 - AAR03929);
9. Gallus gallus (chkhsp?0 - AAR03930);
10. Zea mays (mzehsp?0 - AAR0331);
11. Serratia marcescens (smahsp?0 - AAR03931),
11. Serratia marcescens (smahsp?0 - AAR03932),
having homology to hay 6 f T. vruzi can be used diagnosis involving e.g. Trypanosoma, Mycoplasma
                                                                                                                                                                                                                                                                                               species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the legend of Fig 2, the H. sapiens HSP sequence id residues, the sequence itself has only 640,
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                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus megaterium (Bmehsp70 - AAR03923);
E. coli (dnaK - AAR03924);
                                                                                                                                                                                                                                                                                                                                                                                                      T. cruzi (tc70kd - AAR03925);
T. cruzi (AAR03926);
                                                                                                                                                                                                                                      32.0%;
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Pred. No. 2.1e-189;
0; Mismatches 2;
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             387
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nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 4/4 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic bith predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or progned discovery and for the problem. They are useful for gene discovery and for the problem of the problem of the problem.

New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes

human

The invention relates to a spatially-addressable set of single

ID NO 13330; 327pp + sequence listing;

English.

Claim

27; SEQ

WPI;

2001-496933/54.

Penn (MOLE-)

SG,

Chen W,

Rank

DR.

MOLECULAR DYNAMICS INC Hanzel DK,

agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for

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RESULT 13
ABB30362
ID ABB30
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               Human; microarray;
disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #3013
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNALESYAFNMKSAVEDEGLKGKISEADK
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                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                 2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded by breast cell single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                         single exon
                                                                                                                                                                                                                                                                                                                                                                                                                         probe; gene expression; breast
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RESULT 14
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                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                         measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present semmence is a samples derived from human fetal liver. The present semmence is
fetal liver. The present sequence is a peptide encoded nucleic acid probe of the invention.

Note: The sequence data for this patent did not form paprinted specification, but was obtained in electronic if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the
                                                                                                                     Claim
                                                                                                                                              analyzing
                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                 04-OCT
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #3042 encoded by human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB35536;
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from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                      2001-483447/52
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                                                                                                                      27;
                                                                                                                                                           genome-derived single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168;
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                                                                                                                     SEQ
                                                                                                                                              gene expression
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                        2001WO-US00669
                                                                                                                   ID NO 28171; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression; single exon nucleic acid
                                                                                                                                                                                                               Chen W,
                                                                                                                                              in human
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; Pred. No. 4.4
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
                                                                                                                                                                                                               Rank
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                                                                                                                                                fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   liver single exon probe.
   in electronic format
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                                                                                                                                                         acid probes
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   format directly
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                   probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting disposing grading, staging monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease.
 hypertension, cardiac arrhythmias and congenital heart disease, Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly is
                                                                                                  The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such
                                                                                                                                                        Claim
                                                                                                                                                                                           Single
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30-JUN-2000;
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score greater than or equal to the score of the result being
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Human heat shock p
Human Hsp70 family
Mature mouse sperm
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	73.2	73.6	74.0	74.0	74.7	74.8	75.6	76.7	77.4	81.6	81.6	82.5	83.3	83.9	84.0	84.2	84.2	84.4	85.9	85.9	86.9	87.0	87.6	87.6	87.6	87.6	87.6	87.6	87.6	87.7	87.7	94.8	95.8
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ALIGNMENTS	AAP80088 AAG53605	AAR09418	AAB49099	AAY31380	ABB61529	ABB67209	AAG53604	AAW01638	AAR03932	AAY88412	ABB71708	AAY88413	AAW22895	ABB60514	AAB58386	AAM48711	AAR03930	AAR43002	AAY88410	AAY88409	AAR03928	AAR03927	AAB22938	AAU75102	AAB82535	AAE12987	AAB23651	AAY17407	AAW54364	AAB23649	AAY17408	AAY88411	AAB23650
	Sequence of 70kd p Arabidopsis thalia		Toxoplasma gondii	T. gondii antigen		Drosophila melanog	Arabidopsis thalia	Candida albicans h			melanc	Human heat shock p	Marmoset intracell	Drosophila melanog	Lung cancer associ	Human schizophreni	s gallu	SLIP1 homol	heat shock			Rat HSP (rathsp70)	HSC70	hock	heat	Hsp70	heat s	n heat	S)	heat	heat shock	an heat shock	Rat heat shock pro

AAW54349 RESULT 1 Biochemical markers of human endometrium – useful for, e.g. diagnosis of hyperplasia and adenocarcinoma $\,$ WPI; 1998-207057/18 Byrjalsen I, 08-APR-1997; 06-SEP-1996; 05-SEP-1997; W09810291-A1 Homo sapiens. Endometrium; hyperplasia; adenocarcinoma; proliferative phase; 2D gel electrophoresis; detection. Human heat shock 70 kD protein 1. 14-AUG-1998 (first entry) AAW54349 standard; protein; 641 AA. (CLIN-) CENT CLINICAL & BASIC RES 12-MAR-1998 Fey SJ, 97GB-0007132 96GB-0018600 97WO-GB02394 Larsen Ρ,

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RESULT 2
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Human heat shock protein Hsp70.1 protein sequence SEQ
                                      05-JAN-2001
                                                                                                                   AAB23652 standard;
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Shinbara N,
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                                                                                                                                                                                                                                                                   protozoacide; leukaemia; cancer
                                                                                                                                                                                                                                                                                 cytostatic; immunostimulant; cellular immune response inducer;
                                                               (SUME ) SUMITOMO ELECTRIC IND
2000-543748/49
                                Udono H,
                                                                                                                                  2000WO-JP00941
                                                                                               99JP-0041535
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Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer

Claim Page 46-48; 72pp; Japanese

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The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognissed by cytotoxic T calls and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing the shock protein. Also described are: (1) a drug composition expression vector as active ingression vector (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the exercise workers of (2); and (4) a transformant which can retain the expression vector of (3). (1) has cytostatic, immunostimular and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against Leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention. (I) ψ

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Query Match
Best Local Similarity
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Pred. No. 1.4e-224;
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121 SMVLTKNKEIABAYLGYPVINAVITVPAYFNDSQRQATKDAGVLAGLNVLRIINEPTAAA 180	121 SMYLTKMKETAEAYLGYPYTNAVITVPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA 180	61 LNEQNTVEDAKRLIGREEGDEVVQSDMKHWEFQVINDGDKEKVQVSYKGETKAFYFEEIS 120	61 LNPONTVFDAKRLIGRKFGDPVVQSDMKHWPPQVINDGDKPKVQVSYKGETKAFYPEEIS 120	MAKAAAIGIDLGTTYSCYGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60	MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
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ATPase; Hsp70;

response; infectious

heat shock protein; cytotoxic

disease; malaria; cytotoxic

T lymphocyte;

yte; CTL; T cell;

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RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN 360

RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN

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The invention relates to pharmaceutical compositions comprising peptide binding fragments of heat shock proteins (RESe) and non-covalient complexes of HSP peptide-binding fragments (HEPE) in non-covalient association with antigenic molecules. Vectories comprising peptide fragments of the invention may be used to stimulate an immune response, in particular cytotoxic T cell responses against cells infected with viruses (including hepatitis type A, B and C, influenza, varicella, adenovirus, herpes simplex (HSV) type I and type II, indeepes tin thodorpest ribnovirus, echovirus, respiratory
                                                                                                                                                                                                                                                                                                                                                                                Vaccine compositions for vaccinating against cancers and infections, comprises peptide-binding fragments (PBFs) of heat shock proteins (HSFs) and non-covalent complexes of PBFs of HSFs and antigente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat shock protein; HSP; HSP peptide-binding fragment; HPBF; vaccine; cytotoxic T cell response; hepatitis virus; herpes simplex virus; human immunodeficiency virus; bacteria; Mycobacteria; Rickettsla; protozoa; Leishmani; Trypanosoma; intracellular parasite; Chlamydia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656559/75
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sarcomas and carcinomas, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat qland carcinoma, sebaceous gland carcinoma, papillary carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vystadenocarcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choricoarcinoma, seminoma and embryonal carcinoma. The present sequence is human Hsp70 family homologue, Hsp71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
   RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                   FYEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
                                                                                                                                                 IAYGLDRIGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
                                                                                                                                                                                                                                                 SMVLTKMKEIAEAYLGYPYTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA
                                                                                                                                                                                                                                                                     SMYLTKMKETAEAYLGYPYTNAYITYPAYFNDSQRQATKDAGYTAGLNYLRITNEPTAAA
                                                                                                                                                                                                                                                                                                                                              LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
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                                                     FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
                                                                                                                                                                                                IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3263; DB 22;
Pred. No. 1.4e-224;
; Mismatches 0;
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                                                                                                                              DANGILNYTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN
                                                                                                                                                           DANGILNVTATOKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN
                               QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
                                                              ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
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PTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDI KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI õ

KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI

420

360

420

RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN

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AAB82534 standard; Protein; 641 8

RESULT 4
AABB2534
ID AABI
XX
AC AABI
XX
DT 17-1 AAB82534;

17-SEP-2001 (first entry)

Human

heat shock protein

Hsp71.

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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of human heat shock protein (HSP) HSP/I, an inducible form of a HSP/I family protein. The livertion relates to complexes of peptide-binding fragments of HSPs with antigenic molecules and their use in immunotherapy for the treatment of infectious diseases and cancer. Claimed methods of treating or preventing cancer/infectious diseases involve culturing a cancer cell/infected cell transformed with a nucleic acid encoding a HSP peptide binding domain, recovering complexes of the HSP fragments encovalently associated with peptides from the cancer cell/infected cell, and administering the recovered complexes. These methods can cell, and administering the recovered complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pharmaceutical composition, used to treat or prevent infection or cancer, comprises a complex comprising a heat shock protein-binding fragment associated with a molecule displaying antigenicity of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 46; Fig 1C; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Srivastava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infectious agent or cancer cell -
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                                                                                                                        SMYLTKMKEIAEAYLGYPYTNAVITYPAYFNDSQRQATKDAGYIAGLNYLRIINEPTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
{\tt IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
                          IAYGLDRTGKGERNYLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH
                                                                                                                                                                                            LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
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391.615
/note- "peptide-bind
395.502
/note- "beta-helix m
400.440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "peptide-binding core"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "peptide-binding domain"
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Pred. No. 1.4e-224;
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QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
                                      QVCNPIISGLYQGAGGPGPGGPGAQGPKGGSGSGPTIEEVD 641
                                                                                                               ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
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                                                                                                                                                                                                                                                                             PTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDI
                                                                                                                                                                                                                                                                                                                                       KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
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                                                                                    ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
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RESULT 5 AAB23653 ID AAB2

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AAB23653 standard; protein; 640 8

AAB23653;

05-JAN-2001 (first entry)

heat shock protein Hsp70 protein sequence SEQ Ħ š

protozoacide; APPass: Hsp70; heat shock protein; cytoroxic T lymphocyte; CTL immune response; infectious disease; malaria; cytotoxic T cell cytostatic; lumunostimulant; ccllular immune response inducer; leukaemia; cancer cell;

Homo sapiens

W0200049041-A1

24 - AUG - 2000

18-FEB-2000; 2000WO-JP00941.

19-FEB-1999; 99JP-0041535

Shinbara N, (SUME) SUMITOMO ELECTRIC IND Η,

8

2000-543748/49

Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer

Claim ω, Page 49-52; 72pp; Japanese

γQ

В õ 밁 Š

В ρy 밁

The present invention describes a fused protein (I) prepared from a peptide containing a CTR (cytotoxic T lymphocyte) epitope recognised by peptide containing a CTR (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the APTR set domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as a crive ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3); (1) is a cytostatic, immunostimulant and

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RESULT 6
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Best Local S
Matches 638
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Homo sapiens
                                                                                                     Human; heat shock protein 70;
                                                                                                                                                          Human heat shock protein 70.
                                                                                                                                                                                                                  24-OCT-1997
                                                                                                                                                                                                                                                                                                                        AAW10065 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVCNPIISGi.YQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
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                                                                           ock protein 70; HSP70; primer; probe; detection; abnormal transcription; acute; chronic; sustain
                                                                                                                                                                                                                                                                                                                        Protein;
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Pred. No. 4e-223;
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Best Local Sim
Matches 636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific primer or probe, used chronic sustained stress load
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ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
                                                       DANGILNYTATDKSTGKANKITITNDKGRLSKEEIERMYQEAEKYKAEDEYQRERVSAKN
                                                                                                        PTRQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDI
                                                                                                                                          KSINPDEAVGYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                                                                        KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                                                                                                              RFEHLCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
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)B; AAT58086.
                                     DANGTENVTATOKSTGKANKITITNOKGRESKEETERMVQEAEKIKAEDEVQRERVSAKN
                                                                                         PTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAP-GVPQIEVTFDI
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Pred. No. 3.4e-222;
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Best Local S
Matches 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the human heat shock protein HSP70 mains acid sequence. Human heat shock proteins are located on ohromasomes 69213-7 and 14921-274. The invention relates to the abnormal transcription of introcellular HSP70mRMA under acute and chronic stress load in a human The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress discasses including theumatisms schizophrenia, depression and nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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DB; AAA15620.
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                                                                                                                                            SMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA
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636; Conserv
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d of stress in a human being and ;
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Pred. No. 3.4e-222;
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According to the Legend of Fig 2, the H. saplens HSP sequence has 641 amino acid residues, the sequence itself has only 640, including 'O' (') at position 640.

Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03922);
2. Bacilius megaterium (Emehsp70 - AAR03923);
3. C. coli. (inaK. _AAR03943);
4. C. coli. (inaK. _AAR03943);
5. C. coli. (inaK. _AAR03943);
6. coli. (inaK. _AAR03943);
6. C. coli. (i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins homologous to heat shock proteins from Trypanosoma cruzi - usi in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria
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Human Hsp72; heat shock protein 72; chromosome 6p21 3; Hsp72 inhibitor; expression modulator; JWK phosphatase inhibitor; antiproliferative; drug screening; cancer; leuksemia; lymphoma; solid tumour; sarcoma;
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                                                                                                                                                                                                                                                                                                                                                                                DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN 540
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                                                                                                                                                                                                                                         OVCNPIISGLYQGA-GPGPGGFGAQGPKGGSGSGPTIEEVD 639
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8. Homo sapiens (humbp70 - AAR03929);
9. Gallus gallus (chkhsp70 - AAR03939);
10. Zea mays (mzshsp70 - AAR03939);
11. Serretia marcescens (smahsp70 - AAR03939),
11. Having homology to habp's of T. cruzi can be used in diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   species.
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                                                               shock protein 72).
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Pred. No. 7.2e-221;
2; Mismatches 3;
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Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia,
                                                                                                                     N-PSDB;
                                                                                                                                            WPI; 2000-647056/62
                                                                                                                                                                                                                                                                                      18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                    17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200054814-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma; breast cancer; prostate cancer; premalignant condition.
                                                                                                                                                                                          volloch vz,
                                                                                                                                                                                                                                        (PHYL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Lymphoma
                                                                                                                     AAA97541
                                                                                                                                                                                                                                        PHYLOGENY INC
                                                                                                                                                                                       Sherman
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181 IAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNH 240 	121 SWUTKKKEIAEATIGFPTNAVITVEAYENDSOBOATKDAOVIAGLAVLRIINEPTAAA 180 121 SWUTKKEIAEATIGFPVTNAVITVEAYENDSOBOATKDAOVIAGLAVLRIINEPTAAA 180 121 SWUTKKEIAEATIGFPVTNAVITVEAYENDSOBOATKDAOVIAGLAVLRIINEPTAAA 180	61 LMPONTYEDAKRIJGRKEODPVYOSDMKHMPPOVINGDKPKVOVSYKOETKAEVPBEBIS 120 	1 MAKAAAIGIDLGTTYSCVQVFQHGKVEILANDQGNFTYPSYVAFTDFERLIGDAAKNQVA 60 	Query Match 97.2%; Score 3172; DB 21; Length 624; Best Local Similarity 100.0%; Pred. No. 4.2e-218; Matches 624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 624 AA;	or activity relative to normal levels. The present sequence represents to human Hsp72 used in the exemplifications of the invention.	compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression	and to prevent progression to a neoplastic or malignant state. The	as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit	JNK phosphatase or Hsp72 is used to treat a proliferative disorder such	of HspV2 or JNK phosphatase activity. The compounds identified as inhibitors of HspV2 or JNK phosphatase activity are useful for the safety of	invention additionally encompasses compositions comprising an inhibitor	activation, comprising contacting a test compound with a cert which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits TNV phoenhateon activity. The	complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase activation commission containing a fact commound with a call thich	Optionally, Hep72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a	compound inhibits activity or expression of H	invention rel		Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia, lymphoma	WPI: 2000-647055/62. N-PSDB: AAA97541.	Volloch VZ, Sherman M;	(PHYL-) PHYLOGENY INC.	18-MAR-1999; 99US-0125046.	17-MAR-2000; 2000WO-US07350.	21-SEP-2000.	WO200054814-A1.	Homo sapiens.	carcinoma; breast cancer; prostate cancer; premalignant condition.

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RESULT 10

AARA 3004

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FVEEFKRKHKKDISONKRAVRRLRTACERAKRTISSSTOASLEIDSLFEDIDFYTSITRA
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189..228
/label= IIA
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                                                                                                     "part'
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the ATPase fragment of hsp70 are claimed
                                                                                                                           IIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sulphated glyco-molety interfering composition. The interfering compsn. is e.g. the heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalian fertilisation decrease for detecting and treating infertility — using sulpho glyco lipid immobilishing protein — 1-sulphated-glyco modety interfering compsn., for mycoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                      QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
                                                                               ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQBVISWLDANTLAEKDEFEHKKKELE
                                                                                                                                                               DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN
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                                                               ALESYAFNMKSAVEDEGLKGKLSEADKKKVLDKCQEVISWLDSNTLADKEEFVHKREELE
                                                                                                                                            DANGILNYTATDKSTGKANKITITNDKGRLSKEEIERMVQEAERYKAEDEVQRDRVAAKN
                                                                                                                                                                                                                         PTKQTQTFTTYSDNQPGVLTQVYEGERAMTRDNNLLGRFELSG1PPAPRGVPQ1EVTFDI
                                                                                                                                                                                                                                                                                                         KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                                                                                                                                                                                                                                                             KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI 420
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                                                                                                                                                                                                                                                                                                                                                                                                         RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGHDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNPQNTVFDAKRLIGRKFGDAVVQSDMKHWPFQVVNDGDKPKVQVNYKGESRSFFPEEIS
     DH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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95.2%;
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Pred.
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No. 4.4e-215;
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                                                                                                                                                                                                                                                                                                                        The present invention describes a fused protein (1) prepared from a peptide containing a CTL (cytotoxic T imphocyte) epitope recognised by cytotoxic T calls and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (1) as active ingredient; (2) a DNA encoding (1); (3) anexpression vector containing the DNA of (2); and (4) a transforman which can retain the expression vector of (3). (1) has cytostatic, immunostimulant and protein is useful as an active ingredient for drug inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as mactive ingredient sequence represents a specifically claimed heat shock protein is used in a fixed protein of the present inducer use in a fixed protein of the present inducer use in a fixed protein of the present induced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 39-42; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFPase; Hsp70; heat shock protein; cytotoxic Tymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer;
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                                                 SMYLTKMKETAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNYLRIINEPTAAA 180
                                                                                            LNPQNTVFDAKRLIGRKFGDAVVQSDMKHWPFQVVNDGDKPKVQVNYKGESRSFFPEEIS
                                                                                                                   LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPPQVINDGDKPKVQVSYKGETKAFYPEEIS 120
                                                                                                                                                            MAKNTAIGIDLGTTYSCYGVFQHGKYEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
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                             SMVLTKMKETAEAYLGHPVTNAVITVPAYFNDSQRQATKDAGVTAGLNVLRIINEPTAAA
                                                                                                                                                                                                                                611;
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Pred. No. 9.2e-215;
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                                                                                                                                    Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its applica
                                                                                                                                                                                                                            01-JUN-1995;
                                                                                                                                                                                                                                                   01-JUN-1995;
                                                                                                                                                                                                                                                                             07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                 Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY88411 standard;
                                                                                                                                                                                                                                                                                                     JP2000069999-A
                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                      depression; nephrotic syndrome;
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This sequence represents the human heat shock protein LHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-2 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including

Disclosure; Fig 4; llpp; Japanese.

and its application

rheumatisms,

depression

and nephrotic syndrome

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RESULT 13
AAY17408
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                                                                                                                                                                                                                                 detection;
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                                                                                                                                                                                                                             carcinoma; breast;
                                                                                                                                                                                                                                                          cognate 73; HSC73;
                                                                                                                                                                                                                                                                                                            shock cognate 73
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                                                                                                                                                                                                                                 cancer gene;
tumour.
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                                                                                                                                                                                                                                                          diagnosis; neoplasia;
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FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA

RFEELCSDLFRSTLEPYEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN

360 300 300 SMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA 180

SMYLTKMKETAEAYLGKTYTNAVYTYPAYFNDSQRQATKDAGTTAGLNYLRTTNEPTAAA

LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS

MSKGPAVGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA

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MNPTNTVFDAKRLIGRREDDAVVQSDMKHWPFMVVNDAGRPKVQVEYKGETKSFYPEEVS

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SLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIISWLDKNQTAEKEEFEHQQKELE ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE DANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEKYKAEDEKQRDKVSSKN DANGILNYTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN-540

60C 600 540 481 421 421 361 361 301 301 241

> PTKQTQTFTTYSDNQPGVLTQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDI PTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDI 480 KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI 420 RFEELNADLFRGTLDPVEKALRDAKLDKSQTHDTVLVGGSTRIPKIQKLLQDFFNGKELN

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                                                       Matches 554;
                                                                                                                                                                                                    susceptibility to neoplasia especially malignant neoplasia, and carcinomas of the breast. Gene or protein therapy of mutated H8C73 is performed by administration of native H8C73, and the transgenic mammal is useful as an experimental model for technical development of gene herapy. The H8C73 gene was transfected into call lines, which were introduced into test enimals. These enimals were injected with untransfected cells of a breast cancer ine. Expression of wild type H8C73 prevented breast cancer cells forming tumours in the mice. The present sequence represents mouse H8C73 from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  developed comprising detecting the aberrant expression of a gent
heat shock cognate 73 (HSC73) locus, or detecting a mutation at t
HSC73 locus. The method is used for diagnosing neoplasia or a
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A method of diagnosis performed on a biological sample has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6; 49pp;
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05-NOV-1997;
MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
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                                                                             Similarity
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                                                       Conservative
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97GB-0023412
                                                                          87.7%; Score 2862.5; DB 2
85.8%; Pred. No. 5.7e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
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                                                   47;
                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a fused protein (I) prepared from a pertial containing a CDI (cytotoxic T lamphocyte) eventual recognised by cytotoxic T call and a protein (I) and a protein of a heat shock protein Alsa described a record and III and composition containing (I) as active ingredient. (2) and a recording (II) (3) an expression vector containing the DNA of (3) / ID NA coding III (3) an expression vector (3) / ID NA cytostatic laminum stimulant and the protein of (3) / ID NA cytostatic laminum response compositions are crivities and can be used as a cellular immune response inducer. The protein is useful as restain in information of containing the control of (3) / ID NA cytostatic laminum containing contai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
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Biochemical markers of human endometrium - useful for, diagnosis of hyperplasia and adenocarcinoma
                                                            WPI; 1998-207057/18
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06-SEP-1996;
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Proteins AAW54349-W54364 are examples of proteins produced in endometrium during the hyperplasia, adenocarcinoma or prolifer phase of the endometrium. The presence and quantities of these phase of the endometrium.

proliferative s of these proteins Page 23;

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                                                                                                                                  KSINPDBAVAYGAAYQAAILMGDKSENVQDILLLDVAPLSIGLETAGGVWTALKRNSTI 420
KSINPDBAVAYGAAYQAAILMGDKSENVQDILLLDVAPLSIGLETAGGVWTVLIKRNTTI 420
DANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEKYKAEDEKQRDKVSSKN 540
                                DANGILNYTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN 540
                                                               PTKOTOTETTYSDNOPGVLIQVYEGERANTKONNLLGREELSGIEPAPRGVPDIEVTEDI 480
PTKOTOTETTYSDNOPGVLIQVYEGERANTKONNLLGREELSGIEPAPRGVPQIEVTEDI 480
PTKOTOTETTYSDNOPGVLIQVYEGERANTKONNLLGREELTGIPPAPRGVPQIEVTEDI 480
                                                                                                                                                                                                                           RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN 360
                                                                                                                                                                                                                                                                       FIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRA 300
                                                                                                                                                                                                                                                                                          FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 300
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ALIGNMENTS

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PRELIMINARY; 2002 (TERNHITE1 20, 2002 (TERNHITE1 21, 2002 (TERNHI	PRELIMINARY; PRT; 640 AA. 2002 (TrEMBLIFel. 20, Created) 2002 (TrEMBLIFel. 20, Last sequence updat 2003) amiliaris (Dog) amiliaris (Dog) sheat shock protein 70 (1sp70) mRNA, commed (MOV-2001) to the EMBL/GenBank/DDBJ d kAno R, Hasegawa A.; (1sp70) mRNA, commed (MOV-2001) to the EMBL/GenBank/DDBJ d kB075027; BAB70505.1; - pr0001021; HSP70.1; UNKNOWN_1. pr0001021; HSP70.2; UNKNOWN_1. pr0001022; HSP70.2; UNKNOWN_1. pr0001022; HSP70.2; UNKNOWN_1. pr0001023; HSP70.2; UNKNOWN_1. pr	INARY; PRT; 640 AA. LICEL. 20, Created) LICEL. 20, Last sequence update) LICEL. 21, Last annotation update) 70. Complete Craniata; Vertebrata; Euteleostom; Chordata; Craniata; Vertebrata; Euteleostom; Chordata; Craniata; Vertebrata; Euteleostom; Chordata; Cranidae; Conis. Carnivora; Fissipedia; Canidae; Conis. Carnivora;
	PRT; 640 AA. Created) Last sequence updat Las	PRT: 640 AA. Freated) ast sequence update) ast annotation update) craniata: Vertebrata: Euteleostom. craniata: Vertebrata: Euteleostom. prissipedia; Canidae; Canis. (hbsp70) mRNA, complete cds."; MBL/GenBank/DDBJ databases. MRKOWN.1. RKOWN.1. 40223251871BF87F CRC64: 40223251871BF87F CRC64: 5core 318; DB 6; Length 640: Fred. No. 0; Fred. No. 0; Fred. No. 0; Indels 0; SSNVLTKRWEITAEAYLGYEVTNAVITVPAXFNDS(111111111111111111111111111111111111

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Matches
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Q9UQC1;
01-MAY-2000
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  Q63256 PRELIMINARY
Q63256;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-UN-2002 (TrEMBLRel. 21, Last annotation update)
Heat shock protein 72 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
PRODOM; PD000089; HSP70; 1.
PROSITE; PS00329; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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InterPro; IPR001023; Hsp70.
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                                                                                                                                                 VSILTIDDGIFEVKATAGDTHLGGEDFDNR
                                                                                                                                                                  VSILTIDDGIFEVKATAGDTHLGGEDFDNR
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151 AA;
                                                           PRELIMINARY;
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16473 MW;
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    22,
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    Created)
Last sequence update)
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Best Local :
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                                  TricePro: IP8001033; Hap70.
Pfam: PP00012; HSP70. 1
PRINTS: PR000101; HSP70. 1
PROSTOR: PR0000039; Hsp70. 1
PR0STTE: PS00029; HSP70. 1
PR0STTE: PS00029; HSP70. 1
PR0STTE: PS00029; HSP70. 3; 1.
PR0STTE: PS00029; HSP70. 3; 1.
PROSITE; PSULULUL ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9QWJ5;
Q9QWJ5;
01-MAY-2000
01-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSP70.
                                                                                                                                                                                                                 ROWEN L., MAGAN A., QIN S., HALL J., Dohl T., James R., Schaffer T., RAUCLIFF A., Abbasi N., Loretz C., Lasky Schaffer T., RAUCLIFF A., Abbasi N., Loretz C., Lasky Seguence of the mouse MHC class III region. "Seguence (North-1998) to the PREJCAGENBAN/DOBJ detabases the SIMILARITY: BELONGS TO THE HERT SHOCK PROTEIN 70 FA
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641 AA;
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PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HBP70; 1.
PROSITE; PS00297; HBP70_1; 1.
PROSITE; PS01036; HSP70_3; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. Heat shock protein 70. HSP 70.
                                                                                                                                                                  HSSP; P08107; 1HJO.
MGD; MGI:105975; H2-Bf.
                                                                                                                                                                                                     EMBL; AF109906; AAC84169.1; -.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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373 ANQAAILMODKSENVODILLLIDVAPISGGLETAGGWTALIKRNSTIPTKOTO
373 AAVQAAILMODKSENVODILLLIDVAPISGGLETAGGWTALIKRNSTIPTKOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
    AA;
                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69978 MW;
    70079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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13,
20,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
    F49C33E602EAE334 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641
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STPAIN-MISTAR; TISSUE-SPLEBH, MEDLINE-9410258; PUMPME-8141767; MEDLINE-9410258; PUMPME-8141767; MESILI R., Chi S.H., Sayen M.R., Dillmann W.H.; MESILI R., Chi S.H., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A3A1223439AB2D03 CRC64;
                                                                                                              1.4e-108
                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muridae; Murinae; Rattus
               ç
                                                                                                                                                                                                                             Length
               Indels
                                                                                                                                                                                                                                            641;
               0
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Gaps
               0
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313 TLEPVEKALRDAKLDKAQIHDLVLVGGGTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYG 372 TLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYG 426

426

Last sequence update)
Last annotation update)

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Lasky S.,

Dickhoff R.

SHOCK PROTEIN 70 FAMILY

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AC DT DT DT DT DT DT RN RN RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AN ROWER I... MADAN A., QIN S., Hall J., Dahl T., James R., Dickhof As Schaffer T., Katcliffe A., Abbasi N., Loretz C., Lasky S., Hood T. Sequence of the mouse HRC class III region. The sequence of the mouse HRC class III region. The sequence of the mouse HRC class III region. The sequence of the mouse HRC class III region. The sequence of the mouse HRC class III region. The sequence of the mouse HRC class III region. The sequence of the mouse HRC region. The sequence of the mouse of the sequence of the mouse HRC region. The sequence of the seque
                                                                         O63718 PRELIMINARY; PRT; 455 AA.

O63718;
TOLNOV-1996 (TREMBLrel. 01, Created)
TOLNOV-1996 (TREMBLrel. 01, Last sequence update)
TOLNOV-1996 (TREMBLrel. 01, Last annotation update)
TOLNAR-2002 (TREMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.8%; S
Best Local Similarity 100.0%;
Matches 101; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
SEQUENCE FROM I
Angeletti B., I
d'Ambrosio E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q925V6;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q925V6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSP70
                                                                                                                                                                                                                                                                                                                                                                     198
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                                                                                                                                                                                                                                                                                                                                                               FDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                              PVTNAVITVPAYENDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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1 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                   Passarelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.8%;
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20,
                F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 101; DB 11;
; Pred. No. 3.9e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                   Orru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), DB L1,
3.9e-95;
0;
                   Pascale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                  Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 641;
                Butler R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                               Euteleostomi;
; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Dickhoff R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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075634
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                                                                                            Query Match
Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                      PRIN'S: PRODOL; HEAVESHOCK70.
PRODOM: PRODONO98; HESPO. 1.
PROSITE: PEODO27; HESPO. 2. 1.
PROSITE: PEODO328; HESPO. 2. 1.
PROSITE: PEOLO32; HESPO. 3. 1.
ATP-DAIGNING: HESP. 4. 1.
SEQUENCE: GAI AA: 70437 MW;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, C
01-NOV-1998 (TrEMBLrel. 08, I
01-MAR-2002 (TrEMBLrel. 20, I
Heat shock protein 70 testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1993) to t)
-i- SIMILARITY: BELONGS TO
EMBL; Z27118; CAA81642.1;
HSSP; P08107; 1HJO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      075634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSp70; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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(HSP70)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                        Pfam; PF00012; HSP70;
                                                                                                                                                                                                                                                                                                                                        InterPro: IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                       388 VQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGER 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 THLGGEDFDNRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 GLNVLRIINEPTAAAIAYGLDRIGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 GLNVLRIINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 THLGGEDFDNRLV 238
                                                                                               Local Similarity 100.0%;
nes 72; Conservative
                VQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
73; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of cDNA for
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455 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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455
50405 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 73; DB
&; Pred. No. 2.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation updat
s variant.
                                                                                               Score 72; DB;
; Pred. No. 3.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0F45F12CBA1E2971 CRC64;
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                                                                                                                                                                              303385E7D43019F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      SHOCK PROTEIN 70 FAMILY
                                                                                         DB 4; 40. 3.9e-65; 0;
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2.6e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Inoko H., Fujimoto
HSP70 homolog gene
histocompatibility
                                                                                                                                      Length 641;
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Best Local S
Matches 72
                                                                                                                                                            061698 PRELIMINARY; PRT; 228 AA. 061698; Ol-NOV-1996 (TrEMBLrel. 01, Created) Ol-NOV-1996 (TrEMBLrel. 01, Last sequence update) Ol-NOV-1996 (TrEMBLrel. 1). Last sequence update Heat shock protein (Hsp68) (Fragment).
            "Molecular cloning and analysis of DNA Mr-68,000 heat shock protein mRNAs."; J. Biol. Chem. 261:2102-2112(1986).
                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00012: HSP70: 1.
Probom: PD000089: HSP70: 1.
PROSITE: PS00297: HSP70_1: UNKNOWN_1.
PROSITE: PS00329: HSP70_2: UNKNOWN_1.
PROSITE: PS01036: HSP70_3: UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shiina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,811bp genomic DNA of 6p21.3 HLA class I region.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL. AP000503; BAB63301.;
-InterPro; IPR001023; BAB570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q96QC9;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                        MEDLINE-86111900; PubMed-2868009;
Lowe D.G., Moran L.A.;
                                                                                SEQUENCE FROM N.A.
                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                   HSP70-1.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                AMTKDNNLLGRF
                                                                                                                                                                                                                                                                                                                           VQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGER 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMTKONNLLGRE
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P08109;
                                                                                                                                                                                                                                                                                                                                                                        72;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     641 AA;
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clarity 100.0%;
Conservative
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                                                                                                                Chordata;
Rodentia;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                   70405 MW;
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e EMBL/GenBank/DDBJ
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Last annotation update)
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Pred. No.
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                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Catarrhini; Hominidae;
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                                             complementary to
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OCCORDED DANS

HSP70

Oreochromis mossambicus (Aozambique tilapia) (Tilapia mossambica) Eukaryota, Metazoa: (Dordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthopterygii; Percomorpha;

Perciformes;

Acanthomorpha;

073922 073922; 01-AUG-1998 01-AUG-1998 01-MAR-2002 Heat shock p

(TrEMBLiel.

Created)

07, 20,

Last sequence update)
Last annotation update)

PRELIMINARY;

PRT;

639

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38 (TrEMBLrel.)2 (TrEMBLrel.)protein 70.

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RESULT

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AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNP

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                      Query Match
Best Local S
Matches 58
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Best Local
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01-FBB-1997 (TrEMBLrel. 02, Last sequence update)
01-FMR-2002 (TrEMBLrel. 20, Last senotation update)
70 kba heat-shock protein (Fragment).
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InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
ProDom; PD000089; Hsp70; 1.
NON_TER 1
                                                                                                                                                                              comparisons of a cluster of five HEP70 genes in Fugu rubripes.";
Cell Mol. Life Sci. 55:668-678(1999),
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; 708576; CAA65890.1;
-HSSP; PO8107: 14"
                                                                    ATP-binding.
NON_TER 247
SEQUENCE 247
                                                                                                      PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                    Rigu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordeta; Craniata; Vertebratei; Neoteleostomi; Ratinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                    InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                  Lim E.H., Brenner S.;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99284127; PubMed=10357235;
                                                                                                                                                                                                                                                                                              NCBI_TaxID-31033;
                                                                                                                                                                                                                                                                                                           Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q98896
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AIGIDLGTTYSCYGYFQHGKYEIIANDQGNRTTPSYYAFTDTERLIGDAAKNQYALNP
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                      9.0%;
llarity 100.0%;
Conservative
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26747 MW;
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                      Score 58; DB
Pred. No. 4.9
0; Mismatches
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Pred. No.
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                                                                      1F51A895BC941732 CRC64;
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3.9e-53;
                                   4.9e-51;
                                               DB 13;
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                                             Length 247;
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                        Indels
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                        Gaps
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Euteleostomí; Neoteleostei;

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RESULT 12

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Best Local S
Matches 58
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Best Local S
Matches 58
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Xiphophorus maculatus (Southern platyfish).

Xiphophorus maculatus (Southern platyfish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Meopterygii; Peleostel; Euteleostel; Neoteleosteli Acanthomorpha; Acanthopterygii; Peleoromorpha; Atherinomorpha; Cyprinodontiformes; Poecillidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Stress protein HSP70-2.
                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2001) to the EMBL; AB062114; BAB72168.1; InterPro; IPR001023; Hsp70. Pfam; PF00012; HSP70; 1.
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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Martial J.A., Muller M.,
"Cloning and expression analysis of
tilapia fish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cichlidae; Oreochromis
NCBI_TaxID-8127;
                                                                                                                                                                                                                                                                                                        ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               cultured cells."
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MEDLINE=20291068; PubMed=10828441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Characterization of multiple members of the HSP70 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tamashita M.;
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                                                AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAXNQVALNP
                                                                                          AIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNP
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S; PR00301; HEATSHOCK70
                                                                                                                                                                                                                                 PR00301; HEATSHOCK70.
PD000089; HB970; 1.
PS000297; HS970_1; UNKNOWN_1.
PS000291; HS970_2; UNKNOWN_1.
PS000329; HS970_2; UNKNOWN_1.
PS0003294; T0128 MW; 87382F
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                                                                                                                                                             Similarity
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llarity 100.0%;
Conservative (
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0; Mismatches
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Last annotation update)
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Pred. No.
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hes 0;
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hes 0;
                                                                                                                                                                                       DB 13;
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                                                                                                                                                                                    Length 639;
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Q9R2A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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Q8UWM8;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TERMBLER), Created)
01-MAY-2000 (TERMBLER), 13, Last seque
01-JUN-2002 (TERMBLER), 21, Last annot
Spermatid-specific heat shock protein
MSP70-3 OR HSC70T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                       J. Biochem. 124:347-353(1998).
-: SIMILARITY: BELONGS TO THE EMBL; D85733; BAA32524.1; -.
                                                                                                                                                                                                                                                                           "Genomic structure of the spermatid specific Focated in the class III region of the major complex of mouse and man";
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-129SV/J;
MEDLINE-98351992; PubMed-9685725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xiphophorus maculatus (Southern platyfish).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleos Actinopterygii, Neopterygii, Teleosatai, Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                PRINTS; PR00301; HEATSHOCK70
ProDom; PD000089; Hsp70; 1.
PROSITE; PS00297; HSP70_1; 1
                                                                                                                                       MGD; MGI:96244; Hsp70-3.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9R2A1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSp70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2001) to the EMBL; AB062115; BAB72169.1;
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   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8083;
                      NON_TER
                                             ATP-binding; Heat shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; PS00329; F
; PS01036; F
E 637 AA;
111 AA;
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HSP70_3; UNKNOWN_1.
; 70567 MW; 6B7BD0245141D3A7 CRC64;
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HSP70_1; UNKNOWN_1.
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12137
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Last annotation update)
ck protein 70 (Fragment).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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A1E912BF92630187 CRC64
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1.4e-48;
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HSP70 homolog gene
histocompatibility
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RESULT QBUWMB

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Query Match

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Score 55;

DB 11;

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Search completed: December 4, Job time: 40 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           099KD7 PRELIMINARY; PRT; 633 AA.
099KD7, 01 TIPMILED! 17, Created)
01-JUN-2001 (TIPMILED! 17, Last sequence update)
01-MAR-2002 (TIPMILED: 20, Last annotation update)
Heat shock protein, 70 kDa 2.
ESP70-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mommalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCB_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                               A AIGIDLGTTYSCYGVPOHGKVEIIANDGGHRTPSYVAFTDFERLIGDAAKNOVA 60
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                               2002, 16:52:44
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result heaing printed, and is derived by analysis of the total score distribution.
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        of hits satisfying
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length: 2000000000
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641
1 MAKAAAIGIDLGTT
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     MAKAAAIGIDLGTTYSCVGV
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/cgn2_6/ptodata/J/iaa/5B_coMB.pep:*
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     GenCore version 5.1.3
(c) 1993 - 2002 Compugen Ltd
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US-09-513-78-3-74
US-08-928-52-52
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Million cell updates/sec
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28	Query Matc Best Local Matches	RESULT 1 US-08-441-139-1 US-08-441-139-1 US-08-441-139-1 US-08-441-139-1 US-08-441-139-1 US-08-441-139-1 US-08-441-139-1 US-08-441-139-1 US-08-1441-139-1		444333653228 444321469887
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96523-11 968-441-19-10 Sequence 10, Appl- 109-420-412C-301 Sequence 301, Appl- 109-620-412C-301 Sequence 301, Appl- 109-620-412C-301 Sequence 301, Appl- 109-620-412C-301 Sequence 301, Appl- 108-441-119-5 Sequence 301, Appl- 108-441-119-5 Sequence 5, Appl- 108-441-119-5 Patent No. 519523 Sequence 5, Appl- 108-203-10 Patent No. 519523 P	8.3 100. tive	on US/ , Dr., , Dr., Ann METHIRE RECOLO ESS: 20 ESS: 20 ESS: 21 ESS: 21 ESS: 22 ESS: 23 ESS: 24 ESS: 24 ESS: 25 ESS: 26 ESS: 26 ESS: 27 ESS: 27 ESS: 28 ESS: 2		
96523-11 968-441-19-10 Sequence 10, Appl- 109-420-412C-301 Sequence 301, Appl- 109-620-412C-301 Sequence 301, Appl- 109-620-412C-301 Sequence 301, Appl- 109-620-412C-301 Sequence 301, Appl- 108-441-119-5 Sequence 301, Appl- 108-441-119-5 Sequence 5, Appl- 108-441-119-5 Patent No. 519523 Sequence 5, Appl- 108-203-10 Patent No. 519523 P	٠.	VPP, PP 953 9110 953 11,33		
Patent NO. 5196523 Sequence 10, Appl Sequence 301, App Sequence 301, App Sequence 301, App Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli Sequence 8, Appli Sequence 81, App Sequence 2, Appli Sequence 2, Appli Sequence 31, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 31, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 31, App Sequence 4, App Seque		NANTH HUR HUR Laza MS-10 e #1 /089	>	US-00 US-00
Patent NO. 5196523 Sequence 10, Appl Sequence 301, App Sequence 301, App Sequence 301, App Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli Sequence 8, Appli Sequence 81, App Sequence 2, Appli Sequence 2, Appli Sequence 31, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 31, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 31, App Sequence 4, App Seque	mis	DOS 2008 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LIG	\$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
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Patent NO. 5196523 Sequence 10, Appl Sequence 301, App Sequence 301, App Sequence 301, App Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli Sequence 8, Appli Sequence 81, App Sequence 2, Appli Sequence 2, Appli Sequence 31, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 31, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 31, App Sequence 4, App Seque	DB . 3e	RESSIO	TS	1739- 1720-
Patent No. 5196523 Sequence 301, Appl Sequence 301, Appl Sequence 301, Appl Sequence 40, Appl Sequence 40, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Patent No. 5196523	45.	n SER SI		10 301 301 5 5 5
Patent No. 5196523 Sequence 10, Appl Sequence 301, Appl Sequence 51, Appli Sequence 5, Appli Sequence 5, Appli Repear No. 5196523 Patent No. 5196523 Sequence 41, Appli Sequence 2, Appli Sequence 2, Appli Sequence 41, App	0	PROTE		
Patent No. 5196523 Sequence 10, Appl Sequence 301, Appl Sequence 51, Appli Sequence 5, Appli Sequence 5, Appli Repear No. 5196523 Patent No. 5196523 Sequence 41, Appli Sequence 2, Appli Sequence 2, Appli Sequence 41, App	ingt In	EIN-		
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US-08-797-358B-3
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US-09-513-783A-174
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APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Base
FILE REFERENCE: 99-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
GUIDER TERMAN APPLICATION NUMBER: US/09/513,783A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08797358B Patent No. 6268478
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 180
                                                                                                 TELEFAX: (619) 535-
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r match 8.3%; Score 53; DB 4; Local Similarity 100.0%; Pred. No. 4.2e-45; ses 53; Conservative n. Minmatch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adams, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
STRANDEDNESS: unknown
                                               LENGTH: 643 amino acids
                                                                                                                                                                                         NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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                                  amino acid
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: 1
US-08-928-692-52
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-797-3588-3
                                            US-09-339-972-52
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Sequence 52, Application US/09339972 Patent No. 6323002 GENERAL INFORMATION:
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Patent No.
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                      CLASS.FETCATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE_/DOCKET NUMBER: 4944
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICAMA. METROUS METROUS TITLE OF INVENTION: a Polypeptide TITLE OF INVENTION: a Polypeptide STOUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/928,692 FILING DATE: 12-SEPT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM MEDIUM TYPE: Disketi
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acid
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                                                                                                     211 DGIFEVKATAGDTHLGGEDFDNRLVNHF 238
                                                                                                                               214 DGIFEVKATAGDTHLGGEDFDNRLVNHF 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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ilarity 100.0%;
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                                                                                                                                                                          Score 28;
; Pred. No.
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Pred. No.
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APPLICANT: Brody, Howard

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) MOLECULE TYPE: No. 6323002e US-09-339-972-52
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                                                                                                                                                                                                                                                                                                 Sequence 2, Applicati
Patent No. 5627039
GENERAL INFORMATION:
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TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 52:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                            APPLICANT: Pereira-Smitr
APPLICANT: Wadhwa, Renu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hansen, Kim
TITLE OF INVENTION: Met
TITLE OF INVENTION: a P
                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         214 DGIFEVKATAGDTHLGGEDFDNRLVNHF 241
                                                                                                                                                                                                                                                                                                                                                                                                                       211 DGIFEVKATAGDTHLGGEDEDNRLVNHF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
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OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                CITY: Washington
                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                  COUNTRY:
                                                                                                                                       STATE:
                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/339,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 amino acids
                                                                                                                                                                   E: Howrey & Simon
1299 Pennsylvania Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 Lexington Avenue
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                                                                                                                                                                                                                                                                                 Pereira-Smith, Olivia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: DOS
FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                   MORTALIN AND METHODS FOR DETERMINING COMPLEMENTATION GROUP ASSIGNMENT OF
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Pred. No. 4.6e-2
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US-08-257-073-7
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                                                                                                                                     SOPTWARE: Potentin Release #1.0, Version #1.30
CURRENT ADPLICATION DATA:
APPLICATION MUNEER: US/08/257,073
FILING ADPLICATION: 424
PRIOR APPLICATION MUNEER: US 08/075,783
PRIAM APPLICATION MUNEER: US 08/075,785
APPLICATION MUNEER: US 07/852,305
TILING NOTE: 10:4MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08257073
Patent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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INFORMATION FOR SEQ
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ATTORNEY AGENT INFORMATION:
NAME: AUGTDACH, Jeffrey I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,680 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-383-7451
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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LENGTH: 679 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Frommer, William S. REGISTRATION NUMBER: 25,5
                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Curtis, Morris & Safford,
530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                              UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
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                                                                                                          us 07/672,183
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                             25,506
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                 454310-2570
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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-257-073-7
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Best Local Similarity 100.0%;
Matches 20; Conservative
                                                          Matches
                                                                                      Query Match
Best Local Similarity
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TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-5000
TELEPAY: (617) 526-5000
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 VPQIEVTFDIDANGILNVTA 137
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTMARE: PetentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/066,047A
APPLICATION NUMBER: US/09/066,047A
CLASSITICATION: COMPANDOMPHICATION COMPANDOMPHICAT
                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/044,869 FILING DATE: 25-APR-1997 ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF USE OF GRANULOCYTIC ERHLICHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MURPHY, Cheryl
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                                                          ; 19
                                                                                                                                                                                                                                                                                                                     LENGTH: 649 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: United Stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Superko, Colleen
REGISTRATION NUMBER: 39,850
REFERENCE/DOCKET NUMBER: 106.941.156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BELTZ, Gerald A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
                                                                                  3.0%; Score 19;
100.0%; Pred. No.
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Pred. No.
                                                              Mismatches
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6e-12;
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                                                                                                                 Length 649
                                                          Indels
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US-08-612-302A-37
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Matches 18; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER READABLE
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: LIBM PC COMPARTIBLE
COMPARATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELLEFAX: (1.)
TEX: 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 FKRKHKKDISQNKRAVRR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 APRGVPQIEVTFDIDANGI 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                    STREET: One Westlake
CITY: Valley Forge
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                              ADDRESSEE: Ratner & Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FKRKHKKDISQNKRAVRR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20007-5109
                                                                                                                                                                                                                               One Westlakes, Berwyn
                                                                                                                                                USA
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Sequence 37, Application US/08612302A
Patent No. 5811297 780297
PATENT NO. 5811297 780297
GENERAL INFORMATION: PEFILIPE MEDIATED GENE TRANSFER
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/240,514 FILING DATE: 11-MAY-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Laruner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE-MEDIATED GENE TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73521/102/CLIN
                                                                                                                                                                                                                                                                                    Score 18;
                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                      3.9e-11;
                                                                                                                                                                                                                                                                                  Length 18;
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US-09-632-538C-36
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/ ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3646

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US-09-134-001C-3646
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PRISH: NO. 6440574

CENERAL INFORMATION: PLANT FROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH
TITLE OF INVENTION: PLANT FROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH
TITLE OF INVENTION: LTS USE
TILE REFERENCE: 54359

CURRENT APPLICATION UNMEER: US/09/632,538C

CURRENT PILLING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CENERAL IMPORMATION:

APPLICANT: LYND DOMOSETIC-Stamm et al
TITLE OF INVERTION: SUCCIEC ACID AND ANIMO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVERTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: GTC-007
CUREENT PLUICATION MUNABER: US/09/134,001C
CUREENT FILING DATE: 1997-110-08
PRIOR APPLICATION MUNABER: US/09/134,001C
PRIOR APPLICATION MUNABER: US/09/134,001C
PRIOR APPLICATION MUNABER: US/09/134,001C
PRIOR APPLICATION MUNABER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6380370
                                                                                                                                                 Sequence 36, Application US/09632538C
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3646
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 616
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LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                   464 IPPAPRGVPQIEVTFDID 481
                                                                                                                                                                                                                                   439 IPPAPRGVPQIEVTFDID 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 FKRKHKKDISQNKRAVRR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 7 Mar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FKRKHKKDISQNKRAVRR 18
                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 amino acids
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                                                                                                                                                                                                                                                                                                               2.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                 Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                   Mismatches
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. 1.3e-09;
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3.9e-11;
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US-08-480-190-132
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                                                              Best Loo
Matches
                                                                                            Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                       TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 225 F
CITY: Boston
STATE: Massac
                           38 TPSYVAFTDTERLIGDA 54
                                                            Local Similarity
wes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                amino acid
                                                                                                                                               linear
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 655
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                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudotsuga menziesii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: INH PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                    FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 LSGIPPAPRGVPQIEVTF 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483 LSGIPPAPRGVPQIEVTF 500
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bes 18; Conservation
                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/480,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 Franklin Street
                                                                                                                                                                                                                              (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawrence J. Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mary L. Hedley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roman M. Chicz
Dario A. A. Vignali
2.7%; Score 17; DB 2; I
ilarity 100.0%; Pred. No. 3.8e-10;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert G. Urban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMUNOMODULATORY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                     08/077,255
                                                                                                                                                                                                                                                                                                                                                                              07/925,460
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Pred. No.
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                                    Length 17;
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RESULT 15
PCT-US93-07545-132
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US-08-488-379-132
                                                                                                                                                                                                                                                                                                                                                                                             US-08-488-379-132
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APPLICANT: Roman M. Chicz
APPLICANT: Boman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Stronlinger
                                                                                                                                   Sequence 132, Application PC/TUS9307545 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 132, Application US/08488379 Patent No. 5880103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,255
FILING DATE: JUNE 15,1993
APPLICATION NUMBER: 07/925,460
FILING DATE: AUGUST 11,1992
ATTORNEY/AGENT INFORMATION:
NAME: CLERK, Paul T.

REGISTRATION NUMBER: 30,162
REFERENCE/COCKET NUMBER: 30,0246/168001
TELEPOMUNICATION INFORMATION:
TELEPOME: (617) 542-5970
TELEPOME: (617) 542-5970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                          APPLICANT:
APPLICANT:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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CORRESPONDENCE ADDRESS:
APPLICANT: Jack L. Strominger
TITLE_OF, INVENTION: IMMUNOMODULATORY PEPTIDES
                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                APPLICANT:
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CITY: E
STATE:
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Local Similarity 100.0%;
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CLASSIFICATION: 514
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                                     Roman M. Chicz
Dario A. A. Vignali
Mary L. Hedley
Lawrence J. Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 Franklin Street
                                                                                                                    Robert G. Urban
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                      0; Indels
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PCT-US93-07545-132
                                                                       Query Match
Best Local Similarity 100
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/925.460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEFIONE: (617) 542-5070
RETERENCE: (617) 542-5070
                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50% or 55%x
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: ModPeffect (Version 5.1)
CUMRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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TELEX: 200154
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100.0%; Pred. No. 3.8e-10;
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Search completed: December Job time : 18 secs 4, 2002, 16:53:35 В Ş

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                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compugen Ltd.
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P02824	P82910	P22953	Q10265	P09189	P41826	P41825	001877	P41827				
drosophila	drosophila	arabidopsis	schizosacch	petunia hyb	anopheles a	anopheles a	puccinia gr	anopheles a	schistosoma	caenorhabdi	drosophila	

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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382. MEDLINE-99234376; PubMed-10216320;	Res. 14:8933-8949(1986).	"In vitro transcription of a human hsp 70 heat shock gene by extracts propaged from heat-shocked and non-heat-shocked human cells.";	DESCRIPTION OF 1-22 AND 0.18-041 FROM N.A. MEDINE-87066768; Pubmed-37866141; DESCRIPTION OF A BANGCIA R T. I.	[6]	neat shock protein HSP7U."; Proc. Natl. Acad. Sci. U.S.A. 86:1968–1972(1989).	"Human major histocompatibility complex contains genes for the major		SEQUENCE OF 1-36 AND 360-424 FROM N.A.	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	3 117	SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.	"Sequence of the human major histocompatibility complex class III	Abbasi N., Dicknoff R., Loretz C., Madan A., Dors M., Young J., Tasky S., Hood T.:	James R., Ratcliffe	SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).	Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).	with the nucleotide sequence of human hsp70.";	"Conserved features of eukaryotic hsp70 genes revealed by comparison	MEDLINE-86016721; PubMed-3931075;	UENCE FROM N.A	[2]	"Structure and expression of the three MHC-linked HSP/O genes.";	11-1-1	MEDLINE-91055806; PubMed-1700760;	SEQUENCE FROM N.A.		Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Heat SHOCK /O KDa Procein i (HSP/O.1) (HSP/O.1/HSP/O.2). (HSPAlA OR HSPAl) AND HSPAlB.	15-JUN-2002 (Rel. 41, Last annotation update)	01-FEB-1994 (Rel. 28, Last sequence update)	01-AUG-1988 (Rel 08 Created)	ID HS71_HUMAN STANDARD; PRT; 641 AA.	LT 1	

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MBL, MS9828; AAA632271;

ABAL; MS9800; AAA632271;

ABBL; M134726; AAD2181561;

BMBL, AF134726; AAD2181501;

BMBL, AF134726; AAD2181501;

EMBL, AF100503; BAB6320001;

EMBL, AF000503; BAB632991;

EMBL, M1717; AAA528971;

EMBL, M1717; AAA528941;

EMBL, M1717; AAA528941;

EMBL, M1717; AAA528941;

EMBL, M1717; AAA52811;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00301; HEATSHOCK70.
PRODOM; PD000099; Hsp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001023; Hsp70.
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               61
                                                         61
                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
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                                    LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
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027965; 028122;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
30-MAY-2000 (Rel. 3
                                 KOWBISK J., Gilbert S.A., VAN Drunen-Littel-Van den Hurk S.,
van den Hurk J., Babiuk L.A., Zamb T.J.;
van den Hurk J., Zamb J., Zam
                                                                                                                                                                                                                                                              MEDLINE-94070117; PubMed-8249428;
                                                                                                                                                                                                                                                                                          TISSUE-Liver;
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Grosz M.D., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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35, Last sequence up
39, Last annotation
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PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THE

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Matches 634;
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Best Local
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Probom; PD0000089; HSp70; 1.
PROSITE; PS00229; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Chaperone; Heat : SEQUENCE 641 AA; 70228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U02892; AAA03451.1; -. EMBL; M98823; AAA30568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001023; Hsp70.
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TRAUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS 120
                                               ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE 600
                                                                                                 DANGILNYTATDKSTGKANKITITNDKGRLSKEEIERNYQEAEKYKAEDEVQRERVSAKN
                                                                                                                                                                                PTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDI
                                                                                                                                                                                                                KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                                                                                                                                                               KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                                                                                                                                                                                                 RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                                                                                                                                                                                                                               RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                                                                                                                                                                                                                                                              FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
                                                                                                                                                                                                                                                                                                                                                                   FVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMVLTKWKETAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAA 180
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                  ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
                                                                                                                                                PTKQTQIFTTYSDNQPGVLIQVYEGERAMTRDNNLLGRFELSGIPPAPRGVPQIEVTFDI
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98.9%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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..le-171;
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Query Match
Best Local Similarity
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01-NOV-1997 (Rel. 3
15-JUL-1999 (Rel. 3
Heat shock 70 kDa F
                                             PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat
SEQUENCE 641 AA; 70250 MW.
                                                                                                            Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70
ProDom; PD000089; Hsp70; 1.
PROSTTE; PS00297; HSP70_1; 1.
                                                                                                                                                                                              EMBL; U02891; AAA03450.1; -. HSSP; P08107; 1HJO.
                                                                                                                                                                                                                                EMBL; U09861; AAA73914.1; -.
                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grosz M.D., Skow L.C., Stone R.T.;
"An AluI polymorphism at the bovine (HSP70-1) locus ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95030563; PubMed-7943958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS71_BOVIN
Q27975; Q27964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOVIN
                                                                                                                                                                                InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HSP70-1) locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Angus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 212-641 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
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35, Last sequence up
38, Last annotation
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98.6%;
Score
Pred.
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3216; DB 1;
No. 3.4e-171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE POLIDING OF NEWLY TRANSLATED POLVETTIES IN THE CYTOSOL AS WELL AS WITHIN OFFICIALS. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASHIC RETICULUM FLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING PORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION FATHANAS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY OR RECOGNIZE NOWARTURE COMPORANTIONS OF OTHER PROTEINS. THEY BIND EXTENDED PETIDE SEGMENTS WITH A NET HYROPOPHOBIC CHARACTER REPOSED BY FOLLYEPPTIDES SIGNERYS WITH A NET HYROPOPHOBIC CHARACTER REPOSED BY POLLYEPPTIDES SIGNERING MITCH A NET HYROPOPHOBIC CHARACTER REPOSED BY FOLLYEPPTIDES STREES—INDUCTION: BY HART SHOCK.
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Heat shock; Multigene family.
50 MW; 6D548263E98780F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 kD heat-shock protein-1
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                                                                                                                                                                                                                                                                                                                                                                                                           HS71_PIG
P34930;
01-FEB-1994
01-FEB-1994
01-NOV-1997
Heat shock 7
HSPA1.
Sus scrofa (
                     "Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-280(1992).
-i- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREZEXISTEM: REOTEINS, AGAINST, AGGREGATION AND MEDIATE THE FOLING
OF NUMBLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS HITHIN
ORGANISLICS. THESE CHAPENONES PARTICIPATE IN ALL THESE PROCESSES
THROUGH THEIR ABILITY TO RECORDIZE MONNATURE COMPRANTONS OF
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                       Bouquet
                                                                                                                                                                                                                                   Peelman
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE~92175874;
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
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;; PD000009; HESP70; 1.
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TE; PS00329; HESP70_2; 1.
TE; PS00329; HESP70_3; 1.
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EMBL: X17208: CAM54421;
EMBL: X77208: CAM544221;
EMBL: X77207: CAM54422.1;
EMBL: X747207: CAM54222.1;
EMBL: X747207: CAM52328.1;
HSSP: P08107; 1H30;
InterPro; IPRO0102; HSP70.
Pfam; PF00012; HSP70: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##S71_RAT STANDARD; PRT; 641 A 007435; P42853; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update 16-007-2001 (Rel. 40) Last annotation update Heat shock 70 kDa protein 1/2 (HSP70.1/2).
  ATP-binding; Chaperone;
CONFLICT 71 72
CONFLICT 227 227
                                               PROSITE;
                                                                              ProDom; PROSITE;
                                                                                                                                                                                                                                                        or
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this estatement is only as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Davley; TISSUE-Liver;
MEDLINE-94368974; PubMed-8086479;
LISOWSAR K., KTEWCZYK Z., Widlak W., Wolniczek P., Wisniewski
"Cloning, nucleotide sequence and expression of rat heat induc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Longo F.M., Wang S., Narasimhan P., Zhang J.S., (Massa S.M., Sharp F.R.;
"CDNA cloning and expression of stress inducible and injured rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                       entities requires
                                                                                                                                                                                                                                                                                use by non-profit institutions as long amodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: IN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hsp70 gene.";
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linked heat shock protein 70 (Hi
Immunogenetics 40:325-330(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-LEW.1W/GUN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94096443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  Neurosci.
                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: NO COMERCING WITH OTHER CHAPERONES, HSP70S STABILIZE FUNCTION: IN COMPERCING WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGERGATION AND MEDIATE THE FOLDING OF NERLY TRANSLATED OF LARGE PROTEINS OF NERLY TRANSLATED OF LARGE PROTEINS ARTICLERATE IN ALL THESE PROSESSES THROUGH THEIR ABILITY ON RECORD THE MONARTIE CONFORMATIONS OF THE PROTEINS THEY BIND EXTENDED PROTEINS AND THE PROTEINS AND MEMBRAKE TRANSLATION ON FOLLOWING STRESS-INDUCED DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: BY HEAT SHOCK.
                                             ; PR00301; HEATSHOCK70.

; PD000089; HS970; 1.

TE; PS00297; HS970_1; 1.

TE; PS00329; HS970_2; 1.

TE; PS01036; HS970_3; 1.
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s., Narasimhan P.,
Heat shock; Multigene family.

KR -> NG (IN REF. 3).

D -> H (IN REF. 2 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                three major histocompatibility complex-
(Hsp70) genes of the rat.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ewski J.;
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RESULT 6
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Best Local
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Q28222;
15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
Heat shock 70 kDa |
                                                                                                                                                                                        Eukarya, Metazoa; Chordata; Craniata; Vertebrata; Eutele Manmalia; Eutheria; Prinates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopith
TISSUE-Kidney;

MEDLINE-9508099; PubMed-7988690:

Sainis I, Angelidis C, Pagoulatos G, La

Sainis Hagol gene which is slightly induced

inducible member of the hsp70 gene family
                                                                                                                                                                                                                                                                                               HSPA1.
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FVEEFKRKKKDISONKRAVRLITAGERAKRYLSSSYQASIJEIDSLYGGIDFYTSITRA
FVEEFKRKKKKDISONKRAVRLITAGERAKRYLSSSYQASIJEIDSLYGGIDFYTSITRA
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37, Last sequence up
37, Last annotation
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; Pred. No. 4.4e-168;
13; Mismatches 10;
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Best Local :
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PRINTS; PR00301; HEATSHOCK70.

PRODED: D000089; HSP70; 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00299; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Chaperone: Heat Shock; Multigene family, SEQUENCE 638 AA; 69920 MM; D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the BMBL outstating the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long ass its content is in mo modified and this statement is not removed. Usage by and for commer
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Pfam; PF00012; HSP70; 1.
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                                           419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZIES. THE HSPTOS IN MITOCHONDRIA AND THE ENDPLIASHIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COODERATION WITH HSP90. THEY BARTICITARE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE MONNATIVE DEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPETIDES SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPETIDES SUBJECT, ALTON AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS.INDUCED DAMAGE.
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DANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKN
                                                                                                                                                                                                                  RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
                                                                                                                                                                                                                                                                                              FVEEFKRKHKKDISQNKRAVRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA 60
                                        PTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAP-GVPQIEVTFEI
                                                                           PTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDI
                                                                                                                 KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETPGGVMTALIKRNSTI
                                                                                                                                                         KSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTI
                                                                                                                                                                                               RFEELCSDLFRSTLEPVEKALRDAKLDKAQTHDLVLVGGSTRIPKVQKLLQDFFNGRDLN
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PRINTS; PRO0301; HEATSHOCK70.
PRODOM; PRO00099; HSP70.1; 1.
PROSITE; PS00229; HSP70.2; 1.
PROSITE; PS00229; HSP70.2; 1.
PROSITE; PS00329; HSP70.2; 1.
PROSITE; PS0036; HSP70.3; 1.
ATP-binding; Chaperone; Heat st
COMFLICT 627 627 P
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GENE THROTION: IN COOPEARMION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISSEMENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE POLDING OF NEMLY TRANSLATED POLYPERTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANIZLES. THESE CHAPERONES PRATICIPARE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE MONATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BAND EXTRADED PETTIDE SEMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPERTIDES DURING TRANSLATION
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01-NUC-1999 (Rel. 15, Greated)
01-NUC-1999 (Rel. 35, Last sequence update)
01-NUC-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Heat shock 70 Noa protein 1 (HSP70.1) (HSP70-1/HSP70-2).
HSPA1 ON HSP70A1 OR HSP70-1 OR HCP70.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hunt C., Calderwood S.; "Characterization and sequence of expression in mouse cell lines.";
                                                                                                                               Pfam; PF00012; HSP70; 1.
                                                                                                                                               MGD; MGI:99517; Hsp70-1.
InterPro; IPR001023; Hsp70.
                                                                                                                                                                              PIR; JH0095; JH0095.
HSSP; P08107; 1HJO.
                                                                                                                                                                                                              EMBL; M35021; AAA37864.1;
EMBL; M76613; AAA57233.1;
                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Structure and expression of an inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE~94357449; PubMed~8076831;
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Mammalia; Eutheria;
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P34931, 0900M1.
01-FEB-1094 (Rel. 28, Created)
16-FEB-1094 (Rel. 28, Last sequence of the control of 
                                                                   SEQUENCE PROM. A.
MEDLINE-91055806; PubMed=1700760;
MEDLINE-91055806; PubMed=1700760;
Milner C.M., Campbell R.D.;
"Structure and expression of the
Immunogenetics 32:242-251(1990).
                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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40, Last annotation
protein 1-HOM (HSP70
      Madan
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95.2%; Pred. No. 2e-
tive 20; Mismatches
      Α.,
      Dickhoff R.,
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Catarrhini; Hominidae
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PRINTS; PR00301; HBATSHOCK70.
ProDom; PD000089; HSp70; 1.
PR0SITE: PS00239; HSP70_1; 1.
PR0SITE: PS00329; HSP70_2; 1.
PR0SITE: PS01036; HSP70_3; 1.
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"Sequence of the legion.";
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                     SINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIP
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EMBL; AF134726; AAD21817.1; -
PTR; B45871, B45871.
HSSP; P08107, 1HUO,
Genew; HGNC:5234; HSPA1L.
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V -> A (IN RFT P -> m
                                                                  Score 2921; DI
Pred. No. 7.8e
34; Mismatches
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      MGD: MGI:96231; Hspall.
InterPro: IPRO1023; Hsp70.
Pfam; PF001021; Hsp70.
Pfam; PF001021; Hsp70; 1.
PRINTS: PR00301; HEATSHOCK70.
PRODOM: PD000089; Hsp70; 1.
PROSITE: PS00297; HSP70_1; 1.
PROSITE;
                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the Buropean Bioinformatics Institute as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            HS97_MOUSE STANDARD: PRT: 6
P16627; 061693;
01-MUC-1990 (Rel. 15, Created)
01-FEB-1996 (Rel. 33, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Heat shock 70 kDa-like protein 1.
                                                                                                                                                                                                                                                                    MEDLINE=94299288; PubMed=8026864; Snoek M., Olavesen M.G., van Vugt H.,
                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A. Manuscreece 3302214;
MEDLINE-9014773; PubMed-2302214;
Matsumoto M., Fullmoto H.;
"Cloning of a hap70-ealated gene expressed in mouse spermatids.";
Biochem. Biophys. Res. Commun. 166:43-49(1990).
                                                                                    EMBL; M32218; AAA74906.1; -. EMBL; L27086; AAA59362.1; -.
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                             Campbell R.D.;
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                                                                                                                                                                                                                                                                                                                    Submitted (XXX-1995)
                                                                                                                                                                                                                                                                                                                               Fujimoto
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CNPITKLYQ-SGCTGPTCTPGYTP-GRAATDPTIEEVD
                                      CNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD
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Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID~10116;
                                                                                                               Heat shock 70 kDa
HSP70-3.
MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
                        SEQUENCE FROM N.A.
STRAIN-LEW.1W/GUN;
                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                           STANDARD;
                                                                           Rodentia;
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PROSITE: PS00229; HSP70_2; 1.
PROSITE: PS00229; HSP70_2; 1.
PROSITE: PS00229; HSP70_3; 1.
PROSITE: PS001036; HSP70_3; 1.
ATP-binding: Chaperone: Heat shock: Multigene family.
ATP-binding: Chaperone: Heat shock: Multigene family.
SEQUENCE 641 AA; 70549 MW; 8C77AA9FD98B9252 CRC64;
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linked heat shock protein 70 (HSP70) genes of the rat.";
Immunogenetics 40:325-330(1994).

-i- PUNCTION. IN COOPERATION WITH OTHER CHAPERONES, HSP70S SYMBILIZE
PREZZISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
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NGILNVEAMDKSTGKANKITITNDKGRLSKEEIERMVQEAERYKAEDEGQREKIAAKNAL
                                                                                                                         INPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPT
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                                                        NGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNAL
                                                                                                                                                                                  KQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVTFDIDA
                                                                                                                                                                                                                                                   INPDEAVAYGAAYQAAILMGDKSEKYQDLLLLDVAPLSLGLETAGGVMTYLIKRNSTIPT
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Pred. No. 1.1e-152;
Mismatches 33
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RESULT 11
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                                                                                                                                                                                                                                                                                                                      SPECIES-Mouse: STRAIN-129; TISSUE-Mammary dand; Septimes-Mouse: STRAIN-129; TISSUE-Mammary dand; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                  Giebel L.B., Dworniczak B.P., Bautz E.K.F.;
                                                                                                                                                                                                                                                                                          SPECIES-Mouse;
                                                                                                                                                                                                                                                                                                                                                                                shock-like protein.";
Mol. Cell. Biol. 5:3476-3483(1985).
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-86310827; PubMed-3939319;
O'Mailey K., Mauron A., Barchas J.D., Kedes
"Constitutively expressed rat mRNA encoding
shock-like protein.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sorger P.K., Pelham H.R.B.;
"Cloning and expression of a gene (
Protein in unstressed rat cells.";
EMBO J. 6:993-998(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse), and
Zuiderweg E.R.P.;
"High-resolution
                                               SPECIES=Rat
                                                                                            heat
                                                                                                                            MEDLINE-91067440;
                                                                                                                                                                          Submitted
                                                                                                                                                                                    Hunt C.R.;
                                                                                                                                                                                             SPECIES-Mouse;
                                                                                                                                                                                                                                             encoding
                                                                                                                                                                                                                                                                           MEDLINE=88055872; PubMed=3334718;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=Rat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87246537; PubMed-3595567;
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                       Morshauser R.C., Hu
                                 MEDLINE-99303702;
                                                         STRUCTURE
                                                                                                      Mouse U14 snRNA is encoded in
                                                                                                                 Liu J., Maxwell E.S.;
                                                                                                                                                 SEQUENCE OF 333-383; 438-452 AND
                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                           "Developmental regulation of a constitutively encoding a 72-kDa heat shock-like protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090,
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                                                                               Acids Res.
                                                         BY NMR
                                                                                                                                                                       (NOV-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                125:200-207(1988).
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                      Ξ.
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EMBL; M1192; AAA4335.1;
EMBL; U27129; AAC5336.1;
EMBL; U27129; AAC5386.1;
EMBL; U27144; AAA37869.1;
EMBL; U2744; AAA1391.1;
EMBL; X54401; CAA38267.1;
EMBL; X54402; CAA38268.1;
EMBL; X54402; CAA38268.1;
EMBL; X54403; CAA38269.1;
EMBL; X54403; CAA38269.1;
EMBL; X54403; CAA38269.1;
EMBL; X54403; CAA38269.1;
EMBL; X54403; XA5935,
EMBL; XA5403; XA593
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PRODOM; PD000099; HB970_1: 1.
PROSITE; PS00299; HB970_1: 1.
PROSITE; PS00329; HB970_2: 1.
PROSITE; PS010329; HB970_2: 1.
PROSITE; PS010359; HB970_2: 1.
PROSITE; PS01035; HB970_2: 1
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SWISS-2DPAGE; P08109; MOUSE.
MGD; MGI:105384; HSPA8.
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Pfam; PF00012; HSP70; 1.
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PTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDI
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47; Mismatches
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PIR, A27077, A27077; BSSP; P19120; LARR
SMISSS-2DPAGE; P11142; HUMAN.
AAThuS/Ghent-2DPAGE; 6504; II
PHG1-2DPAGE; P11142; --

HSC-2DPAGE;

P11142;

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                                                                                                                                                                                                                                 SEQUENCE OF 77-86, 221-236 AND 302-311.

MEDILINE-95311348; PubMed-8713105;

Regerton M., Moritz R.L., Druker H., Koron A., Simpson R.J.;

"Identification of the 70kD heat shock cognate protein (Hsc70)

alpha-actinin-1 as novel phosphotyrosine-containing proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dworniczak B.P., Mirault M.-E.;
"Structure and expression of a human
shock 'cognate' protein ";
Nucleic Acids Res. 15:5181-5197(1987)
                                                                                                                                                                                                                Biochem.
                                                                                                                                                                                                                                                                                                     protein database of normal human epidermal keratinocytes.
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                       Vandekerckhove J
                                                                                                                                                                                                                                                                                                                                                 Rasmussen
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Mammalia; Eutheria;
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INDUCTION. CONSTITUTIVELY SYMPHESIZED IN A WIDE VARIETY
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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Catarrhini;
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Best Local
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01-NOV-1990 (Rel. 16, Last seque
16-OCT-2001 (Rel. 40, Last amout
Heat shock cognate 71 kNa protei
Bos taurus (Bovine).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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SEQUENCE 6
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Pfam; PF00012; HSP70; 1.
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWHL outstation - the Burpean Bioinformatics Institute. There are no restrictions on its use by non-profit institute, including the statement is not removed. Usage by and for commercial entities requires a license sgreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  Biochemistry 38:10823-10830(1999)
                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE-99379828; PubMed-10451379;
Johnson E.R., McKay D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sousa M.C., McKay D.B.; "The hydroxyl of threonine 13 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flaherty K.M., Wilbanks S.M., Deluca-Flaherty C.
"Structural basis of the 70 kilodalton heat shock
hydrolytic activity. II. Structure of the active &
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EMBL; X53335; CAA37422.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               protein is essential for transducing
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Chem. 269:12899-12907(1994).
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10-JUL-95
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PROSITE; PS00329; HsP70_1; 1.
PROSITE; PS00329; Hsp70_2; 1.
PROSITE: PS01036; Hsp70_3; 1.
ATP-binding; Heat shock; Mult
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                                                                KVCNPIITKLYQSAGGMPGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD
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                                                                                                        QVCNPIISGLYQGAGG-----PG--PGGF--GAQGPKGGSGSGPTIEEVD
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Pred. No. 4.4e
19; Mismatches
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RESULT 14

HSTC_CRIGR STANDARD; PRT; 646 AA.

110 HSTC_CRIGR STANDARD; PRT; 646 AA.

AC P1978;

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-NOV-1990 (Rel. 39, Last annotation update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Heat shock cognate 71 kDa protein.

GN HSPAG OR HSC70.

GN HSPAG OR HSC70.

OC Cricetulus Griseus (Chinese hamster).

OC Enkaryota; McHazzoa; Chordata; Craniata; Veriebrata; Euteleostomi;

OC Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OX MCBL_TexID-10029;

RN [1]

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PRINTS; PRO0301; HEATSHOCK70.
PRODER: PRO00089; HSp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS00329; HSP70_3; 1.
ATP-binding; Heat shock; Multig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDLINE-90377205; PubMed-1975944;
Ahmad S., Ahuja R., Venner T.J., Gupta R.S.;
*Identification of a protein altered in mutants resistant to
microtubule inhibitors as a member of the major heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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Mol. Cell. Biol.
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INDICTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                          PTKOTQTETTYSONOPGVLIQVYEGERANTKONNLIGRELSGIPPAPGKYQIEVTFOI
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                        ALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
                                                                                   DANGILNYTATDKSTGKANKITITNDKGRLSKEEIERMYQEAEKYKAEDEYQRERYSAKN
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SLESYAFNMKATVEDEKLOGKINDEDKOKILDKCNEIISWLDKNOTAEKEEFEHOOKELE
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5 MW; FC65A2DC5095AD1C CRC64;
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Pred. No. 1.6e-150;
7; Mismatches 43;
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HS70_XENLA
                                                                                                                                                                     Query Match
Best Local S
Matches 551
                                                                                                                                                                                                                           PRINTS; PRO0301; HEATSHOCK70
PRODOM; PRO00089; HESP10.1;
PROSITE; PS00229; HESP10.1; 1.
PROSITE; PS00229; HESP10.2; 1.
PROSITE; PS001036; HESP10.3; 1.
ATP-binding; Heat shock.
SEQUENCE (47 AA); 70915 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS70_XENLA
P02827;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute, where are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Last annotation update)
Heat shock 70 kDa protein (HSP70).
Xenopus laevis (African clawed frog).
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NCBI_TaxID=8355;
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 124
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                               123
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                                                                                                              X01102; CAA25576.1; -.; K02307; AAA49759.1; -. A03310; HHXL70.
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                   VLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIA
 VLTKMKETAEAYLGHPVTNAVITVPAYFNDSQRQATKDAGVLAGLNILRIINEPTAAAIA
                                                        PQNTVFDAKRLIGRKFNDPVVQCDLKHWPFQVVSDEGKPKVKVEYKGEEKSFFPEEISSM
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01, Last sequence update)
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Pred. No. 4.3e-150;
1; Mismatches 35;
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Search completed: December 4, 2002, 16:42:19 Job time : 15 secs

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Minimum
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compugen Ltd
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Sequence 7.5 Appl.
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ALIGNMENTS	US-09-764-868-925	US-09-864-761-42162	US-10-012-756-14	US-10-108-605-129	us-10-108-605-125	US-10-108-605-171	US-09-971-536-72	US-09-864-761-42619	US-09-880-713A-23	US-10-033-026-4	US-10-033-026-6	US-10-033-026-8	US-09-864-761-34320	US-09-864-761-36116	US-09-815-242-13713	US-09-815-242-10015	US-09-759-010-1	US-09-761-534A-6	US-09-761-534A-8	US-09-872-832-29	US-09-815-242-11209	US-09-815-242-12970	US-09-815-242-12567	US-09-815-242-5559	US-09-815-242-10740	US-09-815-242-13682
	Sequence 925, App	Sequence 42162, A	Sequence 14, Appl	Sequence 129, App	Sequence 125, App	Sequence 171, App	Sequence 72, Appl		Sequence 23, Appl	Sequence 4, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 34320, A	Sequence 36116, A	Sequence 13713, A	Sequence 10015, A	Sequence 1, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 29, Appl	Sequence 11209, A	Sequence 12970, A	12567,	Sequence 5559, Ap	Sequence 10740, A	Sequence 13682, A

US-09-759-010-3

Sequence 3, Application US/09759010 Patent No. US20010034042A1

				
181 IAVGLDRTGKGERNVLIFDLGGTFDVSILTIDGIFEVATAGDTHLGGEDFDNRLVHH 241 FVEEFKRKIKKDISONKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA 241 FVEEFKRKHKKDISONKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA	Oy 61_LMPOMYMEDAKELIGRKFGDPYVOSDMKHMPPGVINDGDKPKYVOYSKGETKAFYBEEIS 120	'ative 0 'YSCVGVFQHG	; SEQ ID NO 3 ; LENGTH: 641 ; TYPE: PRT ; ORGANISH: Homo sapiens (US-09-759-010-3) Query Match Best Local Similarity 100.0%; Score 641; DB 10; Length 641; Best Local Similarity 100.0%; Pred. No. 0;	; PRINCE NO. USZULIUJSOZAZAI GENERAL INFORMATION : STIVASLAVA, PRAMOD K. APPLICANN: STIVASLAVA, PRAMOD K. TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPBUTIC AGENTS FILE REFERENCE: 8449-135 FULRENT APPLICATION NUMBER: US/09/759,010 CURRENT APPLICATION NUMBER: US/09/759,010 CURRENT APPLICATION NUMBER: US/09/759,010 NUMBER OF SEQ ID NOS: 11 SOFTWARE: PATEONIT VET. 2.1

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CURRENT PILING DATE: 2001-05-23
PRICOR APPLICATION NUMBER: US 60/207,456
PRICOR PILING DATE: 2000-02-04
PRICOR PILING DATE: 2000-05-26
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TITLE OF INVENTION: UNAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
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                              FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                      FILING DATE: 2001-0
APPLICATION NUMBER:
FILING DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/0066: FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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Hanzel, David K.
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                                                                                                                                                          2001-01-30
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                                                                                                                       PCT/US01/00670
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    09/608,408
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; OTHER INFORMATION: Murine hsp70 US-09-761-534A-10
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ORGANISM: HOMO Septens
FEATURE: INFORMATION: MAP TO API34726.1
OTHER INFORMATION: EXPRESSED IN HBLJOO, SIGNAL - 6.1
OTHER INFORMATION: EXPRESSED IN LING SIGNAL - 15
OTHER INFORMATION: EXPRESSED IN LUNG SIGNAL - 15
OTHER INFORMATION: EXPRESSED IN LUNG MARROW, SIGNAL - 15
OTHER INFORMATION: EXPRESSED IN PLACENAR, SIGNAL - 4.9
OTHER INFORMATION: EXPRESSED IN HPLACENAR, SIGNAL - 7.9
OTHER INFORMATION: EXPRESSED IN HELA SIGNAL - 7.9
OTHER INFORMATION: EXPRESSED IN HELA SIGNAL - 7.9
OTHER INFORMATION: EXPRESSED IN MELA SIGNAL - 3.8
OTHER INFORMATION: EXPRESSED IN MOLT LIVER, SIGNAL - 3.8
OTHER INFORMATION: EXPRESSED IN MOLT LIVER, SIGNAL - 3.8
OTHER INFORMATION: EXPRESSED IN MOLT LIVER, SIGNAL - 3.8
OTHER INFORMATION: EXPRESSED IN MOLT LIVER, SIGNAL - 3.8
OTHER INFORMATION: EXPRESSED IN MALT JODGA - 3.6
OTHER INFORMATION: EXPRESSED IN MALT JODGA - 3.6
OTHER INFORMATION: EXPRESSED IN MALT JODGA - 4.6
OTHER INFORMATION: EXPRESSED INFORMA
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Best Local S
Matches 168
                                                                  NUMBER OF SEQ ID NOS: 25
SOCTWARE: PRESESEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 642
TIPE: PRT
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Patent No. US20020146426A1
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LENGTH: 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Eisen, Herman N.
APPLICANT: Young, Richard A.
TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
TITLE OF INVENTION: Protein Fusion Proteins Maps To A Dis
TITLE OF INVENTION: OA4T Cell-Independent
FILE REFERENCE: 0399.2006-003
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRIOR APPLICATION NUMBER: US 0
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/176,143 PRIOR FILING DATE: 2000-01-14
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ORGANISM: Unknown FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 IEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQR 533
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Palliser, Deborah
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Ani
FILE REFERENCE: PALIGE
CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PC7/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1939-03-12

PRIOR FILING DATE: 1939-03-12
                                                                                                                                                                                                                                  ; Sequence 1519, Application US/09925301
; Patent No. US20020052308A1
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US-09-925-301-1519
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LENGTH: 209
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APPLICANT:
APPLICANT:
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CUBRENT FILING DATE: 201-01-16
PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR PILING DATE: 2000-12-00,776,143
PRIOR APPLICATION NUMBER: US 60/176,143
PRIOR TILING DATE: 2000-01-14
VUMBER: OF SEG DI NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chen, Jianzhu
APPLICANT: Elsen, Herman N.
APPLICANT: Elsen, Herman N.
APPLICANT: Voung, Richard A.
TITHE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
TITHE OF INVENTION: Protein Fusion Proteins Maps To A Dir
TITHE OF INVENTION: CD4-T Cell Independent
TILE REFERENCE: 0399_2006-003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Murine hsp70 - Segment II
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                                                                                                                                                                                                                                                                                                                                                                          111 ARFEELCSDLFR 122
                                                                                                                                                                                                                                                                                                                                                                                                                    300 ARFEELCSDLFR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 HFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 FDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 PYTNAVITYPAYFNDSQRQATKDAGYTAGLNYLRIINEPTAAAIAYGLDRTGKGERNYLI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 11.2%; Score 72; DB 10; Local Similarity 100.0%; Pred. No. 1.1e-60; hes 72; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 HFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cho, Bryan K.
Palliser, Deborah
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                                                                                                                                                               Antibodies
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US-09-870-759-43
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US-09-759-010-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 53
                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SITVASEAVA, PRAMOD K.
TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 43
LENGTH: 646
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GENERAL INFORMATION:
APPLICANT: TERMAN, David S
                                                                           SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                                                                                                Sequence 4, Application US/09759010 Patent No. US20010034042A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1519
LENGTH: 137
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CURRENT APPLICATION MUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
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                                                                                                                FILE REFERENCE: 8449-135
CURRENT APPLICATION NUMBER: US/09/759,010
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEO ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-05-30 NUMBER OF SEQ ID NOS: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1694
              LENGTH: 646
TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (72)
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1 DSGRQATTDAGVIAGLAVLRIINEPTAAAIAYGLDRTGKGERNYLIEDLGGGTFDVSILT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 53; Conserv
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es 71; Conservative
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                                                                                               PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.3%; Score 53; DB 9; Liarity 100.0%; Pred. No. 3.2e-42; Conservative 0; Mismatches 0;
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Pred. No.
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Query Match Best Local Similarity

Conservative

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Gaps

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100.0%;

Score 47; DB 10; Pred. No. 1.6e-36;

Length 665;

7.3%;

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US-09-925-302-724
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                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 886
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 724
LENGTH: 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. US20020044941A1 GENERAL INFORMATION:
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LENGTH: 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: U5/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID SEQUENCES PROWN DEGSOPHILA MELANGASTER THAT ENCODE TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF FILE REFERENCE: 31139 CURRENT APPLICATION NUMBER: US/10/108,605 CURRENT PLILE DATE: 2002-03-27 PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR PRIOR APPLICATION NUMBER: US 60/176,418 PRIOR PRIOR DATE: 2000-01-14 UNIBER: US 60/176,418 PRIOR PRIOR DATE: 2000-01-14 UNIBER: US 60/176,418 PRIOR PLILME DATE: 2000-01-14 UNIBER: US 60/176,418 PLILME DATE: 2000-01-14 UNIB
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                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                        NAME/KEY: SITE
LOCATION: (298)
                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (216)
                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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Bachmann, Jane
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100.0%; Pred. No. 3.2e-42;
tive 0; Mismatches 0;
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100.0%; Pred. No. 3.2e-42
tive 0; Mismatches (
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PRIOR FILING DATE: 2001
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FASTSEQ for W
SEQ ID NO 12058
LENGTH: 637
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                                                                                                                                                                                                                                                        Sequence 35578, Application US/09864761 Patent No. US20020048763A1
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                                                                                                                                                                                                       APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica.*1 CURRENT APPLICATION NUMBER: US/99/864,761
CURRENT APPLICATION NUMBER: US/99/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12058, Application US/09815242
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PYÖKATYÖTES
FILE REFERENCE: ELITRA.011A
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PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                464 IPPAPRGVPQIEVTFDIDANGIL 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind, Judith W.
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100.0%; Pred. No. 8.9e-14;
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FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456

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OTHER INFORMATION: EXPRESSED IN HBLIO, SIGNAL = 54
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN BOUE MARROW, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN BOUE MARROW, SIGNAL = 7.9
OTHER INFORMATION: SAFIGNER - 10.0016 MARROW, SIGNAL = 7.9
OTHER INFORMATION: SAFIGNER - 10.0016 MARROW, SIGNAL = 7.9
                                                                                                                         RESULT 12
US-09-759-010-2
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                           GENERAL INFORMATION:
APPLICANT: Srivast
                                                                      Sequence 2, Application US/09759010 Patent No. US20010034042A1
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      TITLE OF INVENTION:
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SOFTWARE: Annomax Sequence Listing Engine vers.
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BE EILING DATE: 2001-01-19

BE APPLICATION NUMBER: PCT/USO1/00665

BE PILING DATE: 2001-01-30/USO1/00668

BR APPLICATION NUMBER: PCT/USO1/00668

BR FILING DATE: 2001-01-30/USO1/00663
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                              Similarity
Srivastava, Pramod K. VENTION: COMPLEXES OF
                                                                                                                                                                                                                                                                                                                      Conservative
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SWISSPROT HIT: P08109, EVALUE 5.00e-22
EST_HUMAN HIT: BE212199.1, EVALUE 7.00e-21
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100.0%;
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; Pred. No.
   PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
                                                                                                                                                                                                                                                                                                                      Mismatches
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4.7e-09;
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US-09-841-132-301
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; OTHER INFORMATION: Incyte ID No. US20020119463A1 2993696CD1
US-09-919-172-54
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US-09-759-010-2
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SEQ ID NO 54
LENGTH: 654
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                                   NUMBER OF SEC ID NOS: 599

SOFTWARE: PastSEQ for Windows Version 3.0/4.0
SEQ ID NO 301

LENGTH: 183
                                                                                                                                                                                                                                                                                              Patent No. US20020061848A1
                                                                                                                                                                                                                                                                                                                 Sequence 301,
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Matches 16; Conserv
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                                                                                                             APPLICANT: Skeiky, Yasir A.M.
APPLICANT: Dobst, Peter
TITLE DF IMVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE DF IMVENTION: DIAGNOSIS OF CHLANVDIAL INEECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION MUNICE: US/09/841,132
CURRENT FILING DATE: 2001-04-23
CURRENT FILING DATE: 2001-04-23
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APPLICANT: Turner, Christopher M.
TTTLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
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CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
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FILE REFERENCE: 844
                                                                                                                                                                                                                                                     APPLICANT: Bhatia, Ajay
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ORGANISM: Chlamydia
                   TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                             197 RIINEPTAAAIAYGLD 212
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Local Similarity 100.0%;
les 16; Conservation
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100.0%; Pred. No.
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Pred. No. 3.9e-07;
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. 3.9e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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PARENT NO. USAUUAUGUADWAL
GENERAL INFORMATION:
APPLICANT: OALSEA, ROBERT
APPLICANT: Haselbeck, Robert
APPLICANT: OALSEA, ROBERT
APPLICANT: QYNKING JUNGTH W.
APPLICANT: YAMANGER, BOTH
APPLICANT: TYAWICK, JOHN D.
APPLICANT: YAMANGER, BOTH
APPLICANT AND HOWER, BOTH
APPLICANT AND H
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US-09-815-242-11472
US-09-815-242-11472, Application US/09815242
; Sequence 11472, Application US/09815242
; Patent No. US20020061359A1
Search completed: December 4, 2002, 16:56:53 Job time: 12 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-841-132-301
                                                                                                                                                                                                                                                                                                  Query Match 2.3%; Score 15; DB 10; Best Local Similarity 100.0%; Pred. No. 3.3e-06; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.3%; Score 15; DB 10; Best Local Similarity 100.0%; Pred. No. 1.1e-06; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                 472 PQIEVTEDIDANGIL 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 PQIEVTFDIDANGIL 486
                                                                                                                                                      464 PQIEVTFDIDANGIL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 PQIEVTFDIDANGIL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 183;
                                                                                                                                                                                                                                                                                                                                                                                   Length 620;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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>gi|347019|pir||S31716 dnaK-type molecular chaperone hsp72-ps1 - rat
 gi|56385|emb|CAA49670.1| Hsc70-ps1 [Rattus norvegicus]
         Length = 646
 Score = 505 \text{ bits (1301)}, Expect = e-142
 Identities = 259/328 (78%), Positives = 288/328 (87%)
Query: 1 IDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRI 60
          IDSL+EGIDFYTSITRARFEEL +DLFR TL+PVEKALRDAKLDK+QIHD+VLVGGSTRI
Sbjct: 284 IDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAKLDKSQIHDIVLVGGSTRI 343.
Query: 61 PKVQKLLQDFFNGRDLNKSINPDEXXXXXXXXXXXILMGDKSENVQDXXXXXXXXXXXX 120
           PK+QKLLQDFFNG++LNKSINPDE
                                             IL GDKSENVQD
Sbjct: 344 PKIQKLLQDFFNGKELNKSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGI 403
Query: 121 ETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSG 180
           ETAGGVMT LIKRN+TIPTKQTQ FTTYSDNQPGVLIQVYEGERAMTKDNNLLG+FEL+G
Sbjct: 404 ETAGGVMTVLIKRNTTIPTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTG 463
Query: 181 IPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAE 240
           IPPAPRGVPQIEVTFDIDANGILNV+A DKSTGK NKITITNDKGRLSKE+IERMVQEAE
Sbjct: 464 IPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAE 523
Query: 241 KYKAEDEVQRERVSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDA 300
           KYKAEDE QR++VS+KN+LESYAFNMK+ VEDE L+GKI++ DK+K+LDKC E+ISWLD
Sbjct: 524 KYKAEDEKQRDKVSSKNSLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIISWLDK 583
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Query: 301 NTLAEKDEFEHKRKELEQVCNPIISGLY 328

N AEK+EFEH++KELE+VCNPII+ LY

Sbjct: 584 NOTAEKEEFEHOOKELEKVCNPIITKLY 611

12/15/02 11:20 PM

